



FULBRIGHT & JAWORSKI L.L.P.

A REGISTERED LIMITED LIABILITY PARTNERSHIP
600 CONGRESS AVENUE, SUITE 2400
AUSTIN, TEXAS 78701-3271
WWW.FULBRIGHT.COM

DAVID L. PARKER
PARTNER
DPARKER@FULBRIGHT.COM

DIRECT DIAL: (512) 536-3055
TELEPHONE: (512) 474-5201
FACSIMILE: (512) 536-4598

July 26, 2004

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MS Appeal Briefs
Commissioner for Patents
P. O. Box 1450
Alexandria, VA 22313-1450

Re: SN 09/351,778 entitled "Replication Competent Anti-Cancer Vectors"
by Wold et al.
Our ref: INGN:109US

Commissioner:

Enclosed please find the following for filing in the above-referenced patent application:

- (1) Brief on Appeal (original and three copies, with Appendices 1 and 2 and Exhibits 1-5, Exhibit 4 being separately bound);
- (2) \$165 check as the fee for filing the Brief on Appeal; and
- (3) A return postcard to acknowledge receipt of these materials.

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July 26, 2004 Date	 David L. Parker

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Wold *et al.*

Serial No.: 09/351,778

Filed: July 12, 1999

For: Replication Competent Anti-Cancer Vectors

Group Art Unit: 1632

Examiner: Priebe, Scott David

Atty. Dkt. No.: 66153-7775

BRIEF ON APPEAL

MS Appeal Briefs

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

David L. Parker
Attorney for Wold *et al.*
FULBRIGHT & JAWORSKI, LLP.
2400 One American Center
600 Congress Ave.
Austin, TX 78701
(512) 536-5201
dparker@fulbright.com



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APPENDIX 1: Pending Claims on Appeal

APPENDIX 2: Exhibits

Exhibit 1 – Henderson *et al.*

Exhibit 2 – Little *et al.*

Exhibit 3 – Freytag

Exhibit 4 – Wold I Declaration (Separately Bound, with Exhibits A-L)

Exhibit 5 – Wold II Declaration (with Exhibits M-N)



Appellants hereby submit an original and three copies of this Appeal Brief to the Board of Patent Appeals and Interferences in response to the final Office Action dated February 19, 2004. The Notice of Appeal was filed on May 20, 2004, and received in the Patent and Trademark Office on May 24, 2004, making this Appeal Brief due on July 24, 2004.

The fee for filing this Appeal Brief is \$165; a check is enclosed. If the check is inadvertently omitted, or the amount is insufficient, or should any additional fees under 37 C.F.R. §§ 1.16 to 1.21 be required for any reason relating to the enclosed materials, or should an overpayment be included herein, the Commissioner is authorized to deduct or credit said fees from or to Fulbright & Jaworski L.L.P. Account No.: 50-1212/INGN:109US.

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I. REAL PARTIES IN INTEREST

The real parties in interest are St. Louis University (assignee), VirRx (licensee), and Introgen Therapeutics, Inc. (sublicensee).

II. RELATED APPEALS AND INTERFERENCES

There are currently no related appeals or interferences.

III. STATUS OF THE CLAIMS

The application was filed with original claims 1-27. Claims 28-108 were added during prosecution. Of these, claims 1-4, 10, 45-59, 85-96 have been previously cancelled, and claims 6-9, 16-19, 23, 25-31, and 76-84, directed to non-elected species with no currently allowable generic or linking claim, stand withdrawn. Thus, claims 5, 11-15, 20-22, 24, 32-44, 60-75, and 97-108 are pending. Of these, claims 11-15, 20-22, 24, 32-44, 60-75, and 97-108 are subject to the present appeal, with the subject matter of claims 14-15, 24, 62, 63, 67, 70-71 and 100 being free of the prior art. A copy of the appealed claims is attached as Appendix 1.

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IV. STATUS OF AMENDMENTS

No amendments were sought to the pending claims following final rejection.

V. SUMMARY OF THE INVENTION

The present invention is directed generally to the use of a special type of replication-competent “oncolytic” adenoviruses in the treatment of cancer. The oncolytic adenoviruses of the present invention are special in terms of their expression of the ADP gene. The ADP gene (which stands for “adenovirus death protein”) is the gene discovered by the present inventors to promote oncolysis of cancer cells that are infected with these special adenoviruses. The claims can generally be divided into two categories. One category, the “ADP overexpressing” adenovirus claims, are exemplified by claims 13 and 101, and claims depending therefrom:

13. A method for treating cancer in an animal having a tumor comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells and overexpresses an adenovirus death protein (ADP), wherein overexpression is defined as overexpression relative to *dl309*.

101. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells and overexpresses an adenovirus death protein (ADP).

The second category of claims are not per se limited to “ADP overexpression” and are directed to adenoviruses defined in terms of structural instead of functional limitations. This category is exemplified by claim 60 and claims depending therefrom:

60. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector that is replication-competent in neoplastic cells and expresses an adenovirus death protein (ADP), wherein:

- a) the ADP is expressed from an ADP coding sequence positioned under the control of a promoter other than the endogenous promoters for ADP;

- b) the adenovirus vector comprises a deletion in the E3 region that removes a splice site for an E3 mRNA;
- c) the ADP is expressed from an ADP coding sequence flanked by a pre-mRNA splicing and cleavage/polyadenylation signal other than the pre-mRNA splicing and cleavage/polyadenylation signal normally associated with the ADP gene, and/or
- d) the ADP is expressed from an ADP coding sequence that is positioned downstream of the coding sequence for another adenovirus mRNA, together with a sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP.

Lastly, claim 102 specifies ADP overexpression that is achieved by one of the foregoing structural limitations:

102. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells ***and overexpresses an adenovirus death protein (ADP)***, wherein overexpression is effected by one of more of the following modifications:

- a) the ADP is expressed from an ADP coding sequence positioned under the control of a promoter other than the endogenous promoters for ADP;
- b) the adenovirus vector comprises a deletion in the E3 region that removes a splice site for an E3 mRNA;
- c) the ADP is expressed from an ADP coding sequence flanked by a pre-mRNA splicing and cleavage/polyadenylation signal other than the pre-mRNA splicing and cleavage/polyadenylation signal normally associated with the ADP gene, and/or
- d) the ADP is expressed from an ADP coding sequence that is positioned downstream of the coding sequence for another adenovirus mRNA, together with a sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP.

The specification describes a series of exemplary adenoviruses that overexpress ADP, including the KD series (KD1, KD2, KD3) and the GZ series (GZ1, GZ3) and further describes

the use of these vectors in the treatment of human cancer as exemplified through accepted animal models. The KD series include mutations in their E1 regions that appear to limit their replication to cancer cells, whereas the GZ series do not have such limitations. All of these vectors have demonstrated significant if not surprising antitumor oncolytic efficacy. One such vector, designated INGN007, is currently in preclinical development by Introgen Therapeutics, Inc. and is expected to be in the clinic in the very near future.

VI. ISSUES ON APPEAL

This appeal presents the following issues:

- a) Whether the subject matter of the appealed claims is adequately described in the subject specification as required by 35 U.S.C. §112, first paragraph;
- b) Whether the claims 101-102 are indefinite under 35 U.S.C. §112, second paragraph;
- c) Whether the subject matter of claims 10-13, 32-44, 60, 61, 68, 69, 72-75, 97-99 and 101-108 is anticipated by Henderson *et al.* (“Henderson”; Exhibit 1) or Little *et al.* (“Little”; Exhibit 2) under 35 U.S.C. §102(e);
- d) Whether the subject matter of claims 13, 20-22, 60 and 64-66 is obvious under 35 U.S.C. §103 over the combination of Henderson or Little in light of Freytag (Exhibit 3).

VII. GROUPING OF THE CLAIMS

With respect to all of the rejections, the claims shall not stand or fall together and shall be considered separately as set forth hereinbelow. For example, in addition to the groupings set forth by the Examiner, claim 13 and claims depending therefrom shall be considered separately from claim 60 and claims depending therefrom. Furthermore, within these groupings there are

additional claims that are argued separately, including but not limited to claims 68, 70, 72 (which break out individual structural features a) – d) of claim 60), claims 20, 22, 64, 66, (which specify combination therapy with radiation or chemotherapy), claim 101 (ADP overexpression), claim 102 (which specifies ADP overexpression as a function of specified structural limitations), claims 103-106 (which specify methods for measuring overexpression), and claims 107, 108 (which specify human therapy).

VIII. ARGUMENT

A. Rejection of Claims under 35 U.S.C. §112, 1st Paragraph

In the Final Action, claims 11-14, 20-22, 24, 32-62, 64-75 and 85-100 were rejected on the basis of 35 U.S.C. §112, first paragraph, and raises the following issues:

- a) Whether the subject matter of the appealed claims (except, presumably, claims 107 and 108) is adequately described in the specification with respect to the phrase “in an animal having a tumor”;
- b) Whether the subject matter of claims 11-15, 20-22, 24, 32-44 and 108 is adequately described in the specification with respect to the phrase “wherein overexpression is defined as overexpression relative to *dl309*”;
- c) Whether the specification provides written description support for the language “is detectable by western blot, cell lysis, virus release or by cell spreading assay” found in claims 32 and 103-106; and
- d) Whether the specification describes the possibility of including more than one of the four alternatives (elements a) through d)) for upregulating the expression of the adenovirus death protein (“ADP”) set forth in claim 102, claim 60 and claims depending therefrom (claims 60-75 and 97-100, 102).

Appellants will address each of these rejections separately below.

1. ***The subject matter of the appealed claims (except, presumably, claims 107 and 108) is adequately described in the specification with respect to the phrase “in an animal having a tumor”***

a) The Examiner’s Rejection

In the Final Action, the Examiner rejected all of the claims (except, presumably, claims 107 and 108) under §112, first paragraph, taking the position that the specification fails to disclose the treatment of an “animal having a tumor.” The Action acknowledges that the specification does provide support for the treatment of humans having a tumor (claims 107 and 108), but argues that it does not provide written description support for the treatment of animals other than humans. The Action makes reference to the myriad of different types of “animals” that would be embraced by the rejected language.

b) Remarks

In response, Appellants contend that the specification would apprise the skilled artisan that it contemplates treatment of animals with tumors. Thus, the Action’s concern with protozoans and sponges would appear to be unfounded. First of all, the specification is not limited to human tumors and, in fact, contemplates the treatment of “tumors of any origin”:

The invention also provides compositions comprising a recombinant vector that overexpresses ADP in an amount effective for promoting death of neoplastic cells and a method comprising administering a therapeutically effective amount of the vector to a neoplastic cell in a patient. It is believed that the compositions and methods of the present invention ***are useful for killing neoplastic cells of any origin*** and include neoplastic cells comprising tumors as well as metastatic neoplastic cells.

Specification at page 17, lines 16-21 (emphasis supplied). Furthermore, the specification actually sets forth examples of the treatment of animals. This is shown in Examples 4 and 8 of the specification, which demonstrate the treatment of mice having tumors and specifically uses the word “animal” (see specification, page 27, lines 20-21).

The Action's position appears to rely on its interpretation of the meaning of the term "patients" and equates this term with "human patients." However, it is certainly true that an animal can be a "patient," as evidenced by the fact that we have veterinarians and "animal" hospitals.

The Board is therefore requested to overturn the Examiner on this point.

2. ***The subject matter of claims 11-15, 20-22, 24, 32-44 and 108 is adequately described in the specification with respect to the phrase "wherein overexpression is defined as overexpression relative to dl309"***

The Action next takes the position the specification fails to provide written description support for the phrase "wherein overexpression is defined as overexpression relative to *dl309*," found in claims 11-15, 20-22, 24, 32-44 and 108. The Examiner's arguments can be summarized as follows, and the Appellants' response to each follow:

- a) ***That the dl309 adenovirus is not a wild type adenovirus and that there is no evidence that dl309 expresses ADP as high as any previously known adenovirus.***

In response, Appellants note that whether *dl309* is a wild type adenovirus or not, or whether it expresses ADP as high as any previously known adenovirus, is irrelevant to the written description issue. Nevertheless, it is specifically noted that on page 25, lines 28-30, the specification characterizes Ad5, *dl309* and *dl01/07* as "viruses expressing wild-type amounts of ADP." The Examiner has presented no evidence to call into question the objective truth of this statement. *In re Marzocchi*, 439 F.2d 220, 223-24, 169 USPQ 367, 370 (CCPA 1971).

The issue is whether one of skill in the art would understand from the specification that the inventors contemplated that *dl309* was intended to be a standard against which one can measure overexpression. From a review of the specification, there can be no doubt that *dl309* was intended to be just such a standard. This is evident from a reading of the specification at

page 12, lines 18-23 and Example 1. At page 12, lines 18-23, the specification defines “overexpression of ADP” *per se* (as opposed to overexpression relative to *dl309*) to mean that more ADP molecules are made in the infected cell relative to previously known adenoviruses. Example 1 of the specification tests the four exemplary embodiments of the invention, KD1, KD3, GZ1 and GZ3, by comparing their ability to express ADP relative to exemplary previously known adenoviruses, including *dl01/07*, *dl309*, *dl327* and Ad5 (wild type adenovirus). Specification at pages 21-25.

KD1 and KD3 are adenoviral vectors that have the so-called 01/07 mutations in their E1 region that render them replication competent primarily only in neoplastic cells and which further contain deletions in their E3 region that up-regulate ADP expression. GZ1 and GZ3 have the ADP up-regulating E3 mutations, but do not contain the E1 region mutations and thus their replication is not restricted. Contrary to the Examiner’s position in various previous official actions, **ALL** of these vectors, KD1, KD3, GZ1 and GZ3, are representative of the vectors embraced by the claims in that all are replication-competent in neoplastic cells and all have E3 mutations that upregulate ADP expression.

On page 24 of the specification it is also explained that *dl01/07* is the parent vector of KD1 and KD3, except without the ADP-upregulating E3 mutations. Thus, *dl01/07* is replication-restricted to neoplastic cells but do not overexpress ADP. It is also explained that *dl309* is the parent of all of the exemplary vectors of the invention, except that it contains neither the E1 “replication-restriction” mutations nor the ADP up-regulating E3 mutations. Another control vector, *dl327*, is a negative control in that it lacks the ADP gene altogether.

The studies reported on page 24 show that each of the exemplary vectors of the invention overexpress ADP relative to each of the forgoing vectors.

The Examiner's main contention is that the specification allegedly does not state the specific words that dl309 is intended to be a control against which the ADP expression of ALL vectors of the invention are to be measured. However, it is submitted that a fair reading of the specification, from the standpoint of one of skill, is that the vectors were employed in the examples – not just example 1, but in generally each of the examples – for the very purpose of demonstrating what was intended by “ADP overexpression.” Why else were these vectors chosen and presented as ADP expression controls and included as such in virtually all of the examples?

b) That the expression of ADP by dl309 or the KD or GZ vectors was not measured in terms of molecules of ADP per viral genome as per page 12, lines 18-21.

The issue of whether the specification discloses a calculation of the number of molecules of ADP per viral genome is irrelevant to the issue of written description for the rejected phrase, which does not call for such a measurement. The phrase simply refers to overexpression of ADP and the specification describes a number of ways for determining such overexpression, as evidenced by Example 1.

3. The specification does provide written description support for the language “is detectable by western blot, cell lysis, virus release or by cell spreading assay” found in claims 32 and 103-106

The Examiner's main argument, it appears, is that these particular assays for ADP expression levels is only found in the examples for measuring ADP expression with respect to the four exemplary vectors, KD1, KD3, GZ1 and GZ3, and that thus these assays are allegedly not described as a general technique for measuring ADP expression from other vectors within the scope of the claims. With respect to cell lysis assay, the specification analyzes the results of that assay by observing that the assay shows that “over-expression of ADP increases the rate of cell

lysis.” Page 25, lines 18-21. Similarly, with respect to the virus release assay, the specification shows that the assay is capable of distinguishing between viruses “which overexpress ADP” and those “expressing wild-type amounts of ADP.” Page 25, lines 28-30. Likewise, with respect to the cell spreading assay, the specification uses the assay to measure the ability of viruses to lyse cells and spread to newly infected cells and demonstrates “the potency of ADP in mediating ... virus spread in A549 cells.” Page 26, lines 5-6.

With respect to the cell lysis and cell spreading assays, the Examiner states that the example “does not suggest that either assay is to be used to determine whether ADP is overexpressed by a given adenovirus vector used in the invention.” Action at page 5. This is not true. The specification, at page 25, lines 20-21, specifically states that “ADP is required for efficient cell lysis, and over-expression of ADP increases the rate of cell lysis.” This statement is a generalized observation that is, on its face, clearly not limited to the exemplary vectors that were tested. Furthermore, as explained in the first full paragraph of page 26, the cell spreading assay is simply one way of assessing cell lysis (“This result [the cell spreading assay] attests to the potency of ADP in mediating cell lysis and virus spread in A549 cells [the target cells used in the assay].”)

The Examiner’s reliance on the *Purdue Pharma* case is misplaced. In *Purdue Pharma*, the limitation at issue was the so-called C_{\max}/C_{24} ratio which was used in the claims in an attempt to define the class of agents that the claim covered. In the specification at issue there, the C_{\max}/C_{24} ratio was not discussed at all, but merely employed *ex post facto* to characterize two formulations. Nowhere in the patent specification at issue in *Purdue* was it stated that the C_{\max}/C_{24} ratio was intended to be a distinguishing characteristic, with the court characterizing the

C_{\max}/C_{24} ratio as "...a characteristic that is not discussed even in passing in the disclosure ...").
56 U.S.P.Q.2d at 1487.

In contrast, the issue here is the "overexpressing" language and how to interpret that language. There is no question that the specification identifies "overexpression" of ADP as a central focus of the invention, and it is identified throughout the specification as a desirable quality in virtually all embodiments. The question is merely how the specification teaches to measure overexpression, and there are four examples of how to measure overexpression given in Example 1. The Example in no way implies that these four methods are only applicable to KD1, KD2, GZ1 and GZ3 – on the contrary, the specification nowhere says that ADP overexpression is only desirable for these four vectors, and the examples merely provide an example as to how one might proceed to measure ADP expression.

4. ***The specification describes the possibility of including more than one of the four alternatives (elements a) through d)) for upregulating the expression of the adenovirus death protein ("ADP") set forth in claims 60 and claims depending therefrom (claims 60-75 and 97-100, 102).***

The Action next rejects claim 60, alleging that the specification does not provide support for including "more" than one of the indicated adenovirus modifications at a time. Appellants traverse this rejection as well. The Board's attention is directed to the specification at page 13, lines 2-8, particularly at line 5. Appellants agree with the Action that this excerpt presents these four characteristics as alternatives. However, it also presents these characteristics as cumulative and combinable, particularly in light of the fact that the specification specifically employs the inclusive connector "and" when listing the possible elements. See specification at page 13, line 5.

5. Conclusion

For the reasons outlined above, the Board is requested to overturn the Examiner's positions regarding written description.

B. Rejection of Claims Under 35 U.S.C. §112, 2nd Paragraph

The Final Action next rejects claims 101-102 under 35 U.S.C. §112, 2nd paragraph, taking the position that the phrase “overexpresses an adenoviral death protein,” renders the claims unclear as to the metes and bounds of the claim. The Action queries regarding “overexpresses relative to what?” and also states that a “reasonably broad interpretation of these claims would suggest any adenovirus carrying ADP operatively linked to its native promoters” would meet the limitation of the claims.

In response to the Action's query regarding “overexpression relative to what,” Appellants point out that there is a specific definition, at page 12, lines 18-23, for what overexpression is measured against in the context of claims such as claims 101-102 that do not specify the reference virus. Here it is stated that “‘overexpresses ADP’ means that more ADP molecules are made per viral genome present in a dividing cell infected by the vector than expressed by any previously known recombinant adenoviral vector or AAV in a dividing cell of the same type.” As already discussed above, the specification discloses various assays for determining whether more ADP molecules are made per viral genome.

In light of the very clear definition set forth in the specification, the Action's position that a “reasonably broad interpretation of these claims would suggest any adenovirus carrying ADP operatively linked to its native promoters” would meet the limitation of the claims, is not understood. Such an adenovirus would only meet the limitation of the claims if it was shown to express more ADP molecules per viral genome present in a dividing cell infected by the vector

than expressed by any previously known recombinant adenoviral vector in a dividing cell of the same type.

For the foregoing reasons, the Board is requested to overturn the Action's rejections in this regard.

C. Rejection of claims 10-13, 32-44, 60, 61, 68, 69, 72-75, 97-99 and 101-108 is anticipated by Henderson *et al.* ("Henderson"; Exhibit 1) or Little *et al.* ("Little"; Exhibit 2) under 35 U.S.C. §112(e)

The Final Action next rejects claims 10-13, 32-44, 60, 61, 68, 69, 72-75, 97-99 and 101-108 as anticipated by Henderson *et al.* ("Henderson"; Exhibit 1) or Little *et al.* ("Little"; Exhibit 2) under 35 U.S.C. §102(e). The Action takes the position that Henderson and Little both teach an adenovirus, CN751, that has E3 deletions yet retains the ADP gene and thus would be expected to overexpress ADP.

In responding to the rejection, Appellants will provide separate arguments with respect to various claims and will group the claims accordingly.

I. The "Overexpresses ADP" Claims 11- 13, 32-44 and 101-106

Appellants will first address the anticipation rejection with respect to the "overexpressing ADP" claims that have been rejected, which, of those now active, includes claims 11-13, 32-44 and 101-106.

a) It is the Examiner's Burden to Show Anticipation

The Final Action takes the position that it is the Appellants' burden to demonstrate that the CN751 vector of Henderson and Little does not overexpress ADP. Appellants disagree. Since this is an anticipation rejection, the Examiner must demonstrate that each and every element of the claims is either explicitly or necessarily disclosed in the allegedly anticipatory art. That has not been done here. Each of the "overexpresses ADP" claims require *overexpression* of

ADP and there is no teaching anywhere in either Henderson or Little that the vectors they describe overexpress ADP, as that term is used.

The Examiner likens the present situation to the examination of product-by-process claims, where the burden is sometimes shifted to applicants due to the fact that the PTO does not have the necessary laboratories to carry out processes and compare the product so produced against the prior art. However, the situation here is different. The claims specify a particular feature that must be possessed to be within the scope of the claim, and the Examiner has presented no evidence to suggest that the prior art has such a property. To shift the burden to the applicant, examiner's must provide evidence to demonstrate that the prior art "necessarily" has the claimed property. *In re Robertson*, 169 F.3d 743, 745 (Fed. Cir. 1999). As noted by the Federal Circuit, "[i]nherency, however, may not be established by probabilities or possibilities. The mere fact that a certain thing may result from a given set of circumstances is not sufficient." *Id.* at 1269, 20 U.S.P.Q.2d at 1749 (quoting *In re Oelrich*, 666 F.2d 578, 581, 212 U.S.P.Q. 323, 326 (C.C.P.A. 1981)). The Examiner here has not satisfied this burden.

b) CN751 Does Not Overexpress ADP

Furthermore, even if the Examiner has shifted the burden to Appellants to demonstrate that the prior art does not have the claimed property, it is noted that Appellants have done so. Both Henderson and Little teach that CN751 expresses about the same amount of ADP as does wild-type adenovirus, and thus cannot be said to overexpress ADP. This can be seen in Henderson, for example, at col. 49, lines 6-8. Here it is stated that CN751 kills cells more efficiently than an ADP-minus control, but about the same as an ADP-positive wild-type control, Rec700. See also Little *et al.* patent at col. 40, lines 24-26. We know from the present specification that cell killing is a good measure of ADP expression. See Example 2. We also know that *dl309*, the standard against which claim 13 and claims depending therefrom are

measured, expresses “wild-type” levels of ADP. Specification at page 25, lines 28-30. Since we know from Henderson and Little that CN751 expresses wild-type levels of ADP, and in light of the fact that the claims require higher ADP expression than dl309 which expresses wild-type levels, it can be concluded that CN751 does not anticipate these claims.

One of the Action’s responses to this argument is that Appellants have allegedly “indicated on the record (response filed 1/10/02, page 7) that CN751 would be expected to overexpress ADP.” Applicant denies that such a representation was made – the statement referred to by the Examiner was a recitation of the pending rejection that failed to fully attribute the statement to the Examiner. In other words, it was a poorly drafted statement that was never intended to make any admission about what the prior art teaches or does not teach, it simply failed to attribute the statement to the Examiner, which was what was intended. In any event, the question is whether Little or Henderson teaches a vector that overexpresses ADP, and the reality is, as explained above, neither reference teaches overexpression of ADP.

The Action also argues that Henderson/Little teach placing ADP under control of a heterologous promoter (tissue specific or viral promoter), or inclusion of multiple copies of ADP, and that the use of such a heterologous promoter “would be expected to result in overexpression compared to dl309.” In response to the Examiner being requested to set forth the basis for the conclusion that either of these embodiments would result in overexpression, the Action now states that the instant specification teaches, at page 13, that placing ADP under the control of a heterologous promoter is one means of achieving ADP overexpression. However, this position is insufficient: There are all kinds of heterologous promoters, and Henderson/Little are silent as to what kind of heterologous promoter should be used and is silent as to whether the ultimate objective is to achieve overexpression, or even that overexpression of ADP is a

desirable goal. In contrast, Appellants' specification gives an example of a useful heterologous promoter in this regard, the cytomegalovirus promoter.

For the foregoing reasons, it is evident that the Action fails to make out a *prima facie* anticipation of the ADP overexpression claims. (For the sake of completeness, Applicants also incorporate by reference here the comments set forth below with respect to the remaining claims alleged to be anticipated).

c) *The Present Inventors Conceived of Vectors that Overexpress ADP, and their Use in Cancer Therapy, Before the Henderson/Little Priority Date, and Were Diligent in Reducing to Practice*

To demonstrate prior conception and diligence to reduction to practice, Appellants have attached and will rely on two separate declarations of the inventors now on file, including the declaration filed with the response dated 1/6/03 ("Wold I"; Exhibit 4) together with the separately bound exhibits A-L to the Wold I declaration, and the supplemental declaration filed with the response dated September 3, 2003 ("Wold II"; Exhibit 5). It is noted that the Wold II declaration incorporates Wold I in its entirety. See para. 1 of Wold II. The two art references relied upon by the Examiner, Little and Henderson, have a priority date of no earlier than March 3, 1997.

The Research Proposal, Exhibit B to Wold I

We would first direct the Board's attention to Exhibit B of Wold I. This document is a research proposal dated well prior to 3/3/97, and describes the present inventors' goal of preparing adenovirus vectors that overexpress the ADP gene (referred to here as the E3-11.6K gene). In section B of the proposal, the inventors describe the preparation of adenovirus mutants that express the ADP gene, and describe the function of the ADP gene to promote cell death. The inventors note that these earlier studies, using ADP+ and ADP- adenovectors, demonstrated

that the ADP gene indeed functioned to promote cell death in infected cells. Based on these earlier studies, the inventors concluded that “[s]ince the 11.6K protein can promote the cell death of adenovirus-infected, it has the potential use as a therapeutic agent to kill cells, e.g. malignant cell, in humans.” Section B, page 3. Questions are then posed as to how the ADP gene might be applied in human therapy – questions that are addressed in remaining portions of the exhibit.

Turning to page 6 of the Exhibit B research proposal, it is stated that one way to potentially achieve this goal is to construct a vector deleted in the E1A, E1B and E3 regions, wherein the ADP gene is reinserted in an expression cassette driven by the CMV promoter. Page 6, second full paragraph. Then, in section C.3., beginning on page 7, it is alternatively proposed to test the ability of an ADP expressing vector to overexpress the ADP gene (*i.e.*, the 11.6K gene) during early stages of infection by constructing a vector into which the “11.6K gene will be built in” yet which lacks all other E3 region genes and which contains all other adenovirus genes. Such vectors are, in essence, the principal exemplary embodiments of the present invention.

Beginning on page 8, section D., the proposal goes on to suggest the preparation of vectors that “optimize expression” [viz, “overexpress”] of the ADP gene, and mention the possibility of preparing “nondefective” vectors (that is, replication competent vectors).

On pages 9-10 of the proposal, the inventors indicate that they will test the various constructs in animal models to assess their potential efficacy in treating cancer.

Construction and Testing of KD1 Prior to 3/3/97

The Wold I declaration provides additional evidence of conception prior to 3/3/97. In paragraph 5 of Wold I, the inventors detail the following studies conducted prior to 3/3/97:

- the observation that a mutation in the ADP resulted in the slower development of infection as compared to vectors having wild-type ADP;
- the observation that when target cancer vectors prepared with portions of the E3 region removed + reinsertion of the ADP gene resulted in larger plaques, and developed plaques faster, than wild-type (see third bullet point of paragraph 5); and
- gel electrophoresis and immunofluorescence studies demonstrating that E3-deleted, ADP expressing vectors produced higher levels of ADP than wild-type (fourth bullet point of paragraph 5).

Then, in paragraph 6 of Wold I, the inventors provide details on the construction of an ADP overexpressing vector prior to 3/3/97. This is the KD1 vector described in the specification (see, *e.g.*, page 22, Table 1) and which comprises the removal of E3 genes and reinsertion of the ADP gene. In particular, paragraph 6 and the supporting documentation demonstrates that KD1 was actually constructed prior to 3/3/97 and the structure of the E3 region and ADP gene of KD1 was as expected (see, *e.g.*, page 4).

Thus, prior to the filing date of Henderson/Little, the present inventors had conceived of the idea of preparing vectors with E3 deletions + reinsertion of the ADP gene for the purpose of testing overexpression of ADP and for the purpose of developing a cancer therapeutic. Further, they demonstrated that such constructs overexpressed ADP as compared to wild-type and actually prepared the KD1 vector prior to that time. All that remained was testing of the KD1 vector to confirm that it did overexpress ADP (although this had already been shown by them with another such vector) and to show its ability to kill cancer cells in animals. Both of these objectives were diligently attained by the inventors in very short order.

Confirmation that KD1 Overexpressed ADP

Turning now to paragraph 7 of Wold I, the inventors detail studies on KD1 that were conducted in March, April and May of 1997, and present relevant studies that were carried out on KD1 and the KD vectors on virtually every day during those months. In particular, it is shown that at least as early as 5/9/97 to 5/23/97, the inventors conducted plaque assays on KD1 which demonstrated that KD-1 overexpressed ADP. See entries on page 8 of Wold I under the headings "5/9/97 – 5/23/97" and "5/13/97 – 6/2/97".

Successful Animal Testing

The Wold II declaration demonstrates the successful testing of KD1 in an animal having cancer. The inventors there show that on July 7, 1997, they sent KD1, dl1101/1107, dl309, and A549 cells to Dr. Jeffrey A. Whitsett at the Children's Hospital Medical Center, Division of Pulmonary Biology, Cincinnati, OH. A copy of the cover letter sent to Dr. Whitsett is attached to Wold II as Exhibit M. They state that Dr. Whitsett had agreed to test these vectors on their behalf in the A549 nude mouse model, in which A549 human lung carcinoma cells are used to establish tumors in nude mice following by injection of the various vectors to determine their anticancer efficacy. On September 16, 1997, the inventors received a report from Dr. Whitsett's colleague, Lee Zhang, indicating that "10⁹ pfu of each of the viruses were injected into each established A549 tumor. 4 out of 6 tumors injected with KD1 showed slowed tumor growth while 2 out of 2 tumors injected with dl309 and 4 out of 4 injected with dl 1101/1107 continued to grow." A copy of this fax is attached to Wold II as Exhibit N.

From the foregoing it is respectfully submitted that conception + diligence to a reduction to practice has been shown.

In the Final Action, the Examiner raises various points in rebuttal, which Appellants would like to address:

First, in the paragraph bridging pages 10-11, the Action states that Exhibit B to Wold I is merely a research proposal, that it teaches away from using vectors that are “replication competent” in neoplastic cells and that there was no nexus between the Exhibit B proposal and KD1. In response, it is submitted that whether or not the exhibit is a research proposal is irrelevant where, as here, it denotes the inventor’s goal and provides a road map to how they planned to achieve that goal. Further, the proposal does suggest the construction of “nondefective” replication competent vectors at D.1. on page 8. Lastly, while the proposal does not mention KD1 by name, it certainly contemplates the principal attribute of KD1 at issue here – that it comprises an E3-deletion with reinsertion of the ADP gene for “optimization” (*i.e.*, overexpression) of ADP during early stages of infection (as contrasted with late stages).

The Action further states that it was not known prior to 3/3/97 whether KD1 overexpressed ADP. This argument by the Examiner is not particularly relevant in that it overlooks the fact that the declaration DOES demonstrate that the inventors had prepared OTHER vectors with a deleted E3 region and inserted ADP gene, very similar to KD1, and demonstrated that these vectors overexpressed ADP. See bullets 3 and 4 of paragraph 5 of Wold I. Thus, it is clear from the evidence that the inventors had constructed other similar vectors prior to 3/3/97 that were shown to overexpress ADP, and it is evident that it was their intention in preparing KD1 that it have this property as well. It was indeed confirmed to have this desirable property within two months of 3/3/97 after diligent work toward this goal.

The Final Action, at page 11, also takes the position that the declarations do not demonstrate conception of the claimed invention as a whole. This argument is disagreed with on

at least two bases: one, an antedating declaration under Rule 131 need only show so much as the prior art shows, which has been done, and, two, there is no requirement that a Rule 131 declaration demonstrate a reduction to practice of an entire genus.

First, the law is clear that a Rule 131 declaration need only show so much as the prior art discloses. See, *e.g.*, *In re Stempel*, 113 U.S.P.Q. 77 (CCPA 1957). Thus, it is submitted that the present Applicants carried out in the United States studies that demonstrate the reduction to practice of an ADP-overexpressing adenovirus and successful demonstration of tumor growth suppression prior to the March, 1998, effective filing date of the CN751 description in Little/Henderson. Under the doctrine of *In re Stempel*, it is submitted that the Little/Henderson references have been antedated inasmuch as the Rule 131 showing is at least commensurate in scope with that found in the March 1997 and March 1998 respective filing dates of the Henderson/Little patents.

Furthermore, the law is also clear that Rule 131 declarations are not required to set forth a reduction to practice across the claimed genus. For example, in *In re Hostettler*, 148 U.S.P.Q. 514 (CCPA 1966), the court was adamant in reversing the PTO on this very point:

Rule 131 requires applicant to make oath to facts showing a completion "of the invention." That requirement does not mean affiant must show a reduction to practice of every embodiment of the invention. Nor is that requirement coextensive with the amount of disclosure necessary to support a claim under 35 USC 112.

148 U.S.P.Q. at 516.

Furthermore, the fact that Appellants' reduction to practice was demonstrated with a vector having some differences from CN751 in no way undermines Appellants' claim to priority. The fact is, if there are differences, the differences are not relevant to the fundamental issue of who first demonstrated reduction to practice of the central concept of expressing or

overexpressing ADP from a recombinant adenovirus for the purposes of cancer therapy. That showing has clearly been made by the present Applicants. Furthermore, the case law again strongly supports our position. For example, *In re Clarke*, 148 U.S.P.Q. 665 (CCPA 1966), presented the situation where the Rule 131 affidavit described embodiments that were similar to but distinct from the disclosure contained in the reference at issue. In reversing the Board and the examiner, the court observed that:

We believe that Stempel ... is not limited to the fact situations where the inventor can show priority as to the identical compound described in the reference. It seems that in an appropriate case as applicant should not be prevented from obtaining a patent to an invention where a compound described in a reference would have been obvious to one of ordinary skill in that art in view of what the affiant proves was completed with respect to the invention prior to the effective date of the reference.

148 U.S.P.Q. at 670. Here, the fact that Applicants' earlier-reduced-to-practice KD1 included the 01/07 E1 mutation in addition to the upregulating ADP/E3 mutations should thus in no way detract from the ability of KD1 to effectively antedate a reference teaching the ADP/E3 mutations without the 01/07 mutations. Stated another way, KD1 would appear to anticipate or at least obviate CN751, at least to the extent that both are principally concerned with vectors that express ADP as the operative lytic agent.

d) *The Structural Claims – Claims 60, 61, 68, 69, 72-72, 85-87, 89-91 and 94-99*

The Action further rejects structural claims 60, 61, 68, 69, 72-72, 85-87, 89-91 and 94-99 as anticipated by Henderson/Little, noting merely that these claims do not require overexpression of ADP.

Appellants note first that these claims do not require “overexpression” of ADP and are instead directed to the use of vectors having certain structural features. One such feature mentioned in independent claim 60 and dependent claim 72. This feature, directed to adenovirus vectors that express ADP and which “comprise a deletion in the E3 region that removes a splice site for an E3 mRNA,” focuses in on vectors exemplified by the preferred KD and GZ vectors. The foregoing evidence of conception and reduction to practice, incorporated here by reference, applies fully to claims 60 and claims depending therefrom. Furthermore, the fact that these claims do not require overexpression renders irrelevant the Examiner’s argument that KD1 was not shown to overexpress ADP prior to 3/3/97.

Accordingly, for the foregoing reasons, Applicants respectfully request reconsideration and withdrawal of the instant anticipation rejection.

IX. CONCLUSION

Appellants have provided arguments that overcome the pending rejections. Appellants respectfully submit that the Office Action’s conclusions that the claims should be rejected are unwarranted. It is therefore requested that the Board overturn the Action’s rejections.

Please date stamp and return the enclosed postcard to evidence receipt of this document.

Respectfully submitted,



David L. Parker
Reg. No. 32,165
Attorney for Appellants

FULBRIGHT & JAWORSKI
600 Congress Avenue, Suite 240
Austin, Texas 78701
(512) 536-4598

Date: July 26, 2004



APPENDIX 1

PENDING CLAIMS

11. The method of claim 13 wherein the adenovirus death protein comprises SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11 or SEQ ID NO:12.

12. The method of claim 13, wherein the adenovirus vector comprises a recombinant adenovirus lacking expression of at least one E3 protein selected from the group consisting of: gp19K; RID α ; RID β and 14.7K.

13. A method for treating cancer in an animal having a tumor comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells and overexpresses an adenovirus death protein (ADP), wherein overexpression is defined as overexpression relative to *dl309*.

14. The method of claim 13, further comprising the step of passively immunizing the animal against the adenovirus vector.

15. The method of claim 14, wherein the adenovirus vector comprises SEQ ID NO:1 or SEQ ID NO:2.

20. The method of claim 13, further comprising treating the tumor with radiation.

21. The method of claim 20 comprising administering more than one distinct type of recombinant adenovirus to the tumor and treating the tumor with radiation, wherein at least one recombinant adenovirus is replication-defective.

22. The method of claim 13, further comprising treating the tumor with chemotherapy.

24. The method of claim 13, further comprising administering to the tumor one or more replication-defective adenoviruses, wherein each replication-defective adenovirus expresses an anti-cancer gene product, and wherein the adenovirus vector facilitates the spread of the replication-defective adenovirus in the tumor.

32. The method of claim 13, wherein overexpression relative to *dl309* is detectable by western blot, cell lysis, virus release or by a cell spreading assay.

33. The method of claim 13, wherein the adenovirus vector lacks expression of at least one E3 protein selected from the group consisting of gp19K, RID α , RID β and 14.7K.

34. The method of claim 33, wherein the adenovirus vector lacks expression of the gp19K protein.

35. The method of claim 33, wherein the adenovirus vector lacks expression of the RID α protein.

36. The method of claim claim 33, wherein the adenovirus vector lacks expression of the RID β protein.

37. The method of claim 33, wherein the adenovirus vector lacks expression of the 14.7K protein.

38. The method of claim 33, wherein the adenovirus vector lacks expression of the gp19K, RID α , RID β and 14.7K proteins.

39. The method of claim 28, wherein the adenovirus vector comprises a deletion in the E3 region that removes a splice site for any of the E3 mRNAs.

40. The method of claim 13, wherein the adenovirus vector comprises at least one deletion in the E3 region, wherein the at least one deletion comprises a sequence that encodes at

least one E3 protein, wherein the protein is selected from the group consisting of gp19K, RID α , RID β , and 14.7K.

41. The method of claim 40, wherein the at least one deletion comprises a sequence that encodes the gp19K, RID α , RID β and 14.7K proteins.

42. The method of claim 41, wherein the at least one deletion further comprises a sequence that encodes the 6.7K protein.

43. The method of claim 41, wherein the at least one deletion further comprises a sequence that encodes the 12.5K protein.

44. The method of claim 41, wherein the at least one deletion further comprises a sequence that encodes the 6.7K and 12.5K proteins.

60. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector that is replication-competent in neoplastic cells and expresses an adenovirus death protein (ADP), wherein:

- a) the ADP is expressed from an ADP coding sequence positioned under the control of a promoter other than the endogenous promoters for ADP;
- b) the adenovirus vector comprises a deletion in the E3 region that removes a splice site for an E3 mRNA;
- c) the ADP is expressed from an ADP coding sequence flanked by a pre-mRNA splicing and cleavage/polyadenylation signal other than the pre-mRNA splicing and cleavage/polyadenylation signal normally associated with the ADP gene, and/or
- d) the ADP is expressed from an ADP coding sequence that is positioned downstream of the coding sequence for another adenovirus mRNA, together with a sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP.

61. The method of claim 60 wherein the ADP comprises the sequence of SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11 or SEQ ID NO:12.

62. The method of claim 60, further comprising the step of passively immunizing the animal against the adenovirus vector.

63. The method of claim 62, wherein the adenovirus vector comprises SEQ ID NO:1 or SEQ ID NO:2.

64. The method of claim 60, further comprising treating the tumor with radiation.

65. The method of claim 64 comprising administering more than one distinct type of recombinant adenovirus to the tumor and treating the tumor with radiation, wherein at least one recombinant adenovirus is replication-defective.

66. The method of claim 60, further comprising treating the tumor with chemotherapy.

67. The method of claim 60, further comprising administering to the tumor one or more replication-defective adenoviruses, wherein each replication-defective adenovirus expresses an anti-cancer gene product, and wherein the adenovirus vector facilitates the spread of adenoviruses in the tumor.

68. The method of claim 60, wherein the ADP is expressed from an ADP coding sequence positioned under the control of promoter other than the endogenous promoters for ADP.

69. The method of claim 68, wherein the ADP coding sequence is positioned under the control of a promoter that is exogenous to adenovirus.

70. The method of claim 60, wherein the ADP coding sequence is positioned behind a coding sequence for another adenovirus mRNA together with a sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP.

71. The method of claim 70, wherein the sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP is an Ad tripartite leader or a viral internal ribosome initiation sequence.

72. The method of claim 60, wherein the adenovirus vector comprises a deletion in the E3 region that removes a splice site for an E3 mRNA.

73. The method of claim 72, wherein the adenovirus vector lacks expression of at least one E3 protein selected from the group consisting of gp19K, RID α , RID β , and 14.7K.

74. The method of claim 73, wherein the adenovirus vector lacks expression of each of gp19K, RID α , RID β , and 14.7K.

75. The method of claim 74, wherein the adenovirus additionally lacks expression of the E3 6.7K and 12.5K proteins.

97. The method of claim 60, wherein the adenovirus vector is an Ad1, Ad2, Ad5 or Ad6 vector.

98. The method of claim 60, wherein the adenovirus vector is administered to the tumor by injection of vector intravenously or intrathecally.

99. The method of claim 60, wherein the adenovirus vector is administered to the tumor by direct injection of the tumor.

100. The method of claim 60, wherein the animal is passively immunized against the recombinant adenovirus.

101. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells and overexpresses an adenovirus death protein (ADP).

102. A method for treating cancer in an animal having a tumor, the method comprising administering to the tumor an adenovirus vector wherein said adenovirus vector is replication-competent in neoplastic cells and overexpresses an adenovirus death protein (ADP), wherein overexpression is effected by one of more of the following modifications:

- a) the ADP is expressed from an ADP coding sequence positioned under the control of a promoter other than the endogenous promoters for ADP;
- b) the adenovirus vector comprises a deletion in the E3 region that removes a splice site for an E3 mRNA;
- c) the ADP is expressed from an ADP coding sequence flanked by a pre-mRNA splicing and cleavage/polyadenylation signal other than the pre-mRNA splicing and cleavage/polyadenylation signal normally associated with the ADP gene, and/or
- d) the ADP is expressed from an ADP coding sequence that is positioned downstream of the coding sequence for another adenovirus mRNA, together with a sequence on the 5' side of the ADP coding sequence that allows for internal initiation of translation of ADP.

103. The method of claim 32, wherein the overexpression relative to a control virus is detectable by western blot

104. The method of claim 32, wherein the overexpression relative to a control virus is detectable by cell lysis

105. The method of claim 32, wherein the overexpression relative to a control virus is detectable by virus release

106. The method of claim 32, wherein the overexpression relative to a control virus is detectable by a cell spreading assay.

107. The method of claim 60, wherein the animal is a human.

108. The method of claim 13, wherein the animal is a human.

A Novel Three-Pronged Approach to Kill Cancer Cells Selectively: Concomitant Viral, Double Suicide Gene, and Radiotherapy

SVEND O. FREYTAG, KENNETH R. ROGULSKI, DELL L. PAIELLI,
JEFF D. GILBERT, and JAE HO KIM

ABSTRACT

Two obstacles limiting the efficacy of nearly all cancer gene therapy trials are low gene transduction efficiencies and the lack of tumor specificity. Recently, a replication-competent, E1B-attenuated adenovirus (ONYX-015) was developed that could overcome these limitations, because it was capable of efficiently and selectively destroying tumor cells lacking functional p53. In an attempt to improve both the efficacy and safety of this approach, we constructed a similar adenovirus (FGR) containing a cytosine deaminase (CD)/herpes simplex virus type-1 thymidine kinase (HSV-1 TK) fusion gene, thereby allowing for the utilization of double-suicide gene therapy, which has previously been demonstrated to produce significant antitumor effects and potentiate the therapeutic effects of radiation. The FGR virus exhibited the same tumor cell specificity and replication kinetics as the ONYX-015 virus *in vitro*. Importantly, both the CD/5-FC and HSV-1 TK/GCV suicide gene systems markedly enhanced the tumor cell-specific cytopathic effect of the virus, and, as expected, sensitized tumor cells to radiation. By contrast, neither the FGR virus nor either suicide gene system showed significant toxicity to normal human cells. Both suicide gene systems could be used to suppress viral replication effectively, thereby providing a means to control viral spread. The results support the thesis that the three-pronged approach of viral therapy, suicide gene therapy, and radiotherapy may represent a powerful and safe means of selectively destroying tumor cells *in vivo*.

OVERVIEW SUMMARY

In this study, we examine the hypothesis that expression of a CD/HSV-1 TK fusion gene may improve both the efficacy and safety of cancer therapies involving replication-competent, E1B-attenuated adenoviruses. Both the CD/5-FC and HSV-1 TK/GCV suicide gene systems markedly enhanced the tumor cell-specific cytopathic effects of such viruses and sensitized tumor cells to radiation. Neither the virus nor the suicide gene systems showed significant toxicity to normal human cells. Both suicide gene systems were effective at suppressing viral replication, thereby providing a safety mechanism to halt virus spread. We propose that the three-pronged approach of viral therapy, suicide gene therapy, and radiotherapy may ultimately prove to be a safe and effective means of selectively destroying tumor cells *in vivo*.

INTRODUCTION

DESPITE ADVANCES IN BOTH diagnosis and therapy, the annual number of cancer-related deaths has not decreased during the past 60 years. Although conventional cancer therapies (surgery, radiotherapy, chemotherapy) produce a high rate of cure for patients with early-stage disease, many cancers recur and the majority of patients with advanced cancer eventually succumb to the disease. The limitations of conventional cancer therapies do not derive from their inability to ablate tumor, but rather from limits on their ability to do so without excessively damaging the patient. It is this consideration that constrains the extent of surgical resection, the dose of radiation and volume to be irradiated, and the dose and combination of chemotherapeutic drugs. Improving the effectiveness of a treatment is of no clinical value if there is no significant increase

in the differential response between tumor and normal tissue (*i.e.*, the therapeutic index).

As a means of increasing the therapeutic index, several new approaches involving gene therapy are under development. One of these approaches, suicide gene therapy, involves the transfer and expression of nonmammalian genes encoding enzymes that convert nontoxic prodrugs into toxic antimetabolites. Two suicide genes currently being tested in clinical trials are the *Escherichia coli* cytosine deaminase (CD) and herpes simplex type-1 thymidine kinase (HSV-1 TK) genes, which confer sensitivity to 5-fluorocytosine (5-FC) and ganciclovir (GCV), respectively (DeClercq, 1984; Calabresi and Chabner, 1990). The rationale behind the suicide gene therapy approach is that, following targeted transfer of these genes to the tumor site, only the tumor and neighboring cells (via bystander effects) will be rendered sensitive to their cytotoxic action. Thus, with this approach, systemic toxicity commonly associated with, and a major limitation of, conventional chemotherapy [*e.g.* 5-fluorouracil (5-FU)] is avoided. We (Rogulski *et al.*, 1997b) and others (Moolten and Wells, 1990; Moolten, 1994; Ezzeddine *et al.*, 1991; Culver *et al.*, 1992; Mullen *et al.*, 1992, 1994; Huber *et al.*, 1993, 1994; Takamiya *et al.*, 1993; Chen *et al.*, 1994; Hirschowitz *et al.*, 1995; Richards *et al.*, 1995; Cool *et al.*, 1996; Dong *et al.*, 1996; Ohwada *et al.*, 1996) have demonstrated the efficacy and safety of suicide gene therapy in animal models. Using retrovirally transduced cells, we have achieved 100% regression of very large intramuscular tumors (3 cm³) using the CD/5-FC and HSV-1 TK/GCV systems simultaneously with no side effects (Rogulski *et al.*, 1997b). It is noteworthy that the size of these experimental tumors is within the range of those observed in human cancer patients. These results give us reason to believe that the suicide gene therapy approach could be efficacious against some human tumors providing that the genes can be delivered efficiently to the tumor site. Unfortunately, a current limitation of nearly all cancer gene therapy approaches is that the efficiency at which therapeutic genes can be delivered *in vivo* is too low to make them efficacious against most human cancers.

A novel approach with much potential is the use of replication-competent, mutant adenoviruses that preferentially replicate in tumor cells (Bischoff *et al.*, 1996; Heise *et al.*, 1997). The prototype ONYX-015 is a replication-competent mutant adenovirus that fails to express the 55-kD E1B protein, which binds to and inactivates the cellular tumor suppressor p53 (Yew and Burke, 1992). As a result, this virus replicates in, and preferentially kills, cells lacking functional p53. The strength of this approach is that it exploits a major biological difference between normal and tumor cells, which should result in an increase in the therapeutic index. Moreover, the replication capacity of the virus should dramatically increase the efficiency of its antitumor effect. However, despite its noted strengths, this approach has limitations. For example, there is no reason to think that E1B-attenuated viruses, such as ONYX-015, could selectively destroy tumors cells containing functional p53. This point may be important, because many human tumors exhibit significant intratumoral heterogeneity with respect to p53 status (Mirchandani *et al.*, 1995; Yang *et al.*, 1996). Because adenoviruses are immunogenic, this approach will elicit an immunological response that may not only attenuate its antitumor effects, but may also preclude repeated doses. Finally, the ability of the virus to replicate, albeit ineffi-

ciently, in normal human cells, may raise concerns regarding the safety of this approach. Thus, it would be desirable to combine this approach with one that could (i) expand the spectrum and tumor cell types that it would be effective against, (ii) increase its therapeutic efficacy per dose, and (iii) control the replication and spread of the virus.

With these goals in mind, we developed a replication-competent, E1B-attenuated adenovirus similar to ONYX-015 that contains a CD/HSV-1 TK fusion gene. We demonstrate here that this virus exhibits all the advantages of the ONYX-015 virus, but in addition, is improved significantly in both efficacy and safety.

MATERIALS AND METHODS

Plasmids, viruses, antibodies, and cell lines

All plasmids containing adenoviral sequences used in the construction of a replication-competent, E1B-attenuated adenovirus containing a CD/HSV-1 TK fusion gene (FGR) were obtained from Microbix (Toronto, Canada). Construction and characterization of the CD/HSV-1 TK fusion gene has been previously described (Rogulski *et al.*, 1997a). Wild-type adenovirus type 5 and ONYX-015 were obtained from ONYX Pharmaceuticals (Richmond, CA). U251, DU145, PC-3, HT29, and MRC-5 cells were obtained from the American Type Culture Collection (ATCC). 293 cells were obtained from Microbix. Antibodies to the adenovirus type 2 E1A (sc-430) and 55-kD E1B (DP08) proteins were obtained from Calbiochem (LaJolla, CA).

Construction of FGR and production of adenoviruses

The wild-type E1 region from bases 343 to 2,270 was generated by the polymerase chain reaction (PCR) using pXC1 (Microbix) as template. The resulting 1,928-bp fragment contained *Bam* HI restriction sites at each end, a *Bgl* II restriction site 5' to the 3' *Bam* HI site, and two mutations at bases 2,253 (C → T) and 2,262 (G → T) generating premature translation stop codons in the 55-kD E1B reading frame at codons 79 and 82, respectively. The PCR fragment was digested with *Bam* HI and cloned into the 6.4kb fragment of pCA14 (Microbix) generating pCA14-E1aE1b. The CD/HSV-1 TK fusion gene was removed from pWZLneoCDglyTK (Rogulski *et al.*, 1997a) by a partial *Bam* HI-*Eco* RI digestion and cloned between the *Bam* HI and *Eco* RI sites of pCA14 generating pCA14-CDglyTK. The entire expression cassette, containing the cytomegalovirus (CMV) promoter, CDglyTK fusion gene and SV40 polyadenylation elements, was removed from pCA14-CDglyTK by *Bgl* II digestion. The 3.1-kb fragment was cloned into the sole *Bgl* II site of pCA14-E1aE1b generating pCA14-E1aE1b/CDglyTK. Both pCA14-E1aE1b/CDglyTK and pCA14-CDglyTK were linearized with *Pvu* I and co-transfected with *Cla* I-linearized pBHG10 (Microbix) into 293 cells to generate the FGR virus and its replication-defective counterpart (Ad5-CDglyTK). Isolated plaques were picked 10–14 days later and plaque-purified on 293 cells a second time. All viruses were propagated in 293 cells to generate crude viral supernatants (titers 20–20 × 10⁸ pfu/ml) or CsCl gradient-purified virus (titers 5–50 × 10¹¹ pfu/ml). All viral preparations were assayed for their ability to

replicate in and lyse non-E1A-expressing cells, for genome integrity and stability by Southern blotting, and for expression of the CDglyTK fusion gene by Western blotting and immunofluorescence.

Western blotting

Cells (1×10^6 , 60-mm dish) were infected with the various crude viral supernatants at an multiplicity of infection (moi) of 10 in 0.2 ml of Dulbecco's modified Eagle's medium (DMEM). After 1 hr, fresh growth media was added. Eighteen hours post-infection, cells were lysed in Laemmli sample buffer. Samples (15 μ l) containing protein from 3×10^5 cells were applied to a SDS-10% polyacrylamide gel and transferred to nitrocellulose using standard procedures. Blots were probed with a polyclonal antibody directed against the adenovirus type 2 E1A protein (sc-430). Antibody binding was visualized using standard chemilluminescence procedures.

Cytosine deaminase assays and immunofluorescence

Cells (1×10^6 , 60-mm dish) were harvested 48 hr post adenoviral infection. Cell extracts were prepared and cytosine deaminase (CD) assays performed as previously described (Rogulski *et al.*, 1997a). For each reaction, 50 μ g of protein was used. For CD immunofluorescence, tumors were excised, frozen, and sectioned. Samples were placed on glass slides, fixed in methanol, and washed thoroughly with phosphate-buffered saline (PBS). Samples were incubated with a polyclonal antibody to *E. coli* CD (provided by C. Richards, Glaxo-Wellcome), followed by a Texas Red-conjugated donkey anti-rabbit antibody. Samples were stained with DAPI and photographed using an Olympus fluorescent microscope.

Immunoprecipitation

For immunoprecipitation of the adenovirus 55-kD E1B protein, cell monolayers were incubated in 4 ml of DMEM containing 2% dialyzed fetal calf serum (FCS) and 100 μ Ci/ml [35 S]methionine/cysteine (ICN, TRANS 35 SLABEL; 1,439 Ci/mmol) for 2 hr beginning 16 hr post-infection. Cell monolayers were washed with PBS and lysed directly in 1 ml of RIPA buffer (9.1 mM NaH₂PO₄, 1.7 mM NaH₂PO₄, 150 mM NaCl, 1% Nonidet P-40, 0.5% Na deoxycholate, 0.1% SDS pH 7.4). Cell extracts were clarified by microcentrifugation, and preabsorbed with 1 μ g of normal rabbit serum and 20 μ l of Protein A/G PLUS Agarose (Santa Cruz Biotechnology Inc.). One microgram of the monoclonal anti-55-kD E1B antibody (DP08) was added to 0.5 ml of clarified cell extract and incubated on ice for 1 hr. Twenty microliters (20 μ l) of Protein A/G PLUS Agarose was added and the sample was incubated at 4°C for 1 hr with constant mixing. The immunoprecipitates were collected by microcentrifugation and washed four times with 1 ml of RIPA buffer followed by one wash with 1 ml of PBS. The final pellet was resuspended in 40 μ l of Laemmli sample buffer, heated at 100°C for 5 min, and the agarose was pelleted by microcentrifugation. Twenty microliters of the supernatant fractions were applied to an SDS-10% polyacrylamide gel and the dried gel were subjected to autoradiography.

Cytopathic effect (CPE)

To compare the viral cytopathic effects, cells (10^5 /well, 24-well plate) were either mock-infected, or infected with increasing moi in 0.2–0.4 ml of DMEM. After 1 hr, the virus was removed and cells were incubated in DMEM containing 10% FCS (growth medium). Duplicate plates were fixed and stained with crystal violet either 5 or 9 days post-infection. For prodrug sensitivity assays, cells (1×10^6 , 60-mm dish) were either mock-infected, or infected with virus at an moi of 10. After 1 hr, the cells were detached and replated (2×10^4 cells/well, 24-well plates) in either growth medium, or growth medium containing varying concentrations of prodrugs (GCV and/or 5-FC). The media was changed every 2 days. Duplicate plates were fixed and stained with crystal violet either 5 or 9 days later. To quantify the cytopathic effect, cells were replated in triplicate at low density (10^4 and 10^3 cells/60-mm dish) immediately following infection. Colonies were fixed, stained with crystal violet, and counted 7–10 days later.

Assay for viral replication

Cells (1×10^5 /well, 24-well plate) were either mock-infected, or infected at an moi of 10 in 0.2 ml of DMEM. After 1 hr, the virus was removed and cells were incubated in DMEM containing 10% FCS. Cells were harvested every day thereafter by lysing them in 0.4 ml of 10 mM Tris-HCl pH 7.5, 10 mM NaCl, and 0.6% SDS. Genomic DNA was precipitated by the addition of 0.1 ml of 5 M NaCl and incubation at 4°C overnight. Following microcentrifugation, the supernatant fractions were extracted with phenol, CHCl₃, and viral DNA was precipitated with ethanol. Samples were digested with *Hind* III and analyzed by Southern blotting using standard techniques. The blots were probed with [32 P]pBHG10 (Microbix), which detects all but the left-most *Hind* III fragment of all the viruses. To monitor prodrug inhibition of viral replication, cells (1×10^6 , 60-mm dish) were infected with FGR at a moi of 10 and immediately replated (2×10^4 cells/well, 24-well plate) in varying concentrations of prodrugs. Cells were harvested 48 hr post-infection and processed for Southern blot analysis as described above.

Radiosensitivity experiments

DU145 and U251 cells (2×10^5 cells/well, 6 well plate) were either mock-infected, or infected with FGR at a moi of 1. Cells were incubated in growth medium for 48 hr to allow for viral replication and expression of the CD/HSV-1 TK fusion gene. The medium was then replaced with normal growth medium or medium containing either 40 μ g/ml of 5-FC or 0.1 μ g/ml of GCV. After 24 hr, cells were exposed to a single dose of γ -irradiation (0–6 Gy). Cells were immediately replated in triplicate at low density (1×10^4 and 1×10^3 cells/60-mm dish) in growth medium. Colonies were fixed, stained with crystal violet, and counted 7–10 days later. The sensitizer enhancement ratio (SER) represents the ratio between the D_0 of radiation alone and the D_0 for radiation plus virus and prodrugs. Cell survival data were analyzed using a nonlinear least square algorithm (Albright, 1987). Radiation cell survival curves were fit using the Single-Hit Multi-Target (SHMT) model.

RESULTS

Characterization of replication-competent, E1B-attenuated adenovirus containing CD/HSV-1 TK fusion gene

A schematic representation of the E1 region of our replication-competent, E1B-attenuated adenovirus containing the CD/HSV-1 TK fusion gene (FGR) is shown in Fig. 1. Expression of the CDglyTK gene (Rogulski *et al.*, 1997a) is driven by the human CMV promoter and utilizes simian virus 40 (SV40) polyadenylation elements. The entire expression cassette is situated within an intron in the adenovirus E1B region immediately downstream of the 19-kD E1B gene. FGR expresses the wild-type adenovirus type 5 E1A and 19-kD E1B proteins. Two premature translation stop codons were placed in the 55-kD E1B gene that would result in the production of a truncated 78-amino acid protein. This truncated protein does not contain the p53 binding domain (amino acids 215–354, Yew and Burke, 1992; Kao *et al.*, 1990), and therefore cannot interact with p53. FGR also contains a 2.68-kb deletion in the E3 region (bases 28,133–30,181).

To demonstrate that FGR had the expected properties, virus-infected DU145 prostate adenocarcinoma cells were examined

for expression of the E1A and 55-kD E1B proteins, virus replication, and CD activity (*i.e.*, expression of the CDglyTK fusion protein). FGR produced similar amounts of the E1A proteins as wild-type adenovirus type 5 and ONYX-015 (Fig. 2A). However, like ONYX-015, it failed to express the 55-kD E1B protein (Fig. 2B). FGR replicated in DU145 cells with kinetics similar to that of wild-type adenovirus and ONYX-015 (Fig. 2C); however, it and ONYX-015 replicated slightly slower than wild-type virus in most other tumor cell types examined (*e.g.*, U251, HT-29; not shown). The titer (pfu) of virus produced in one cycle "burst" assays correlated well with the steady-state levels of viral DNA observed in the Southern blots (not shown). The replicative capacity of FGR subsequently resulted in high expression of the CDglyTK fusion protein as determined by CD assays. Seventy-two hours post-infection, FGR expressed the CDglyTK protein at a level 50-fold greater than a stably, retrovirally transduced cell line and 300-fold greater (after correcting for differences in moi) than cells infected with Ad5-CDglyTK, a replication-defective version of FGR (Fig. 2D). This clearly illustrates the advantage of a replication-competent adenovirus over a nonreplicating adenovirus (*i.e.*, greater therapeutic gene expression per dose).

To demonstrate that FGR, like ONYX-015, preferentially

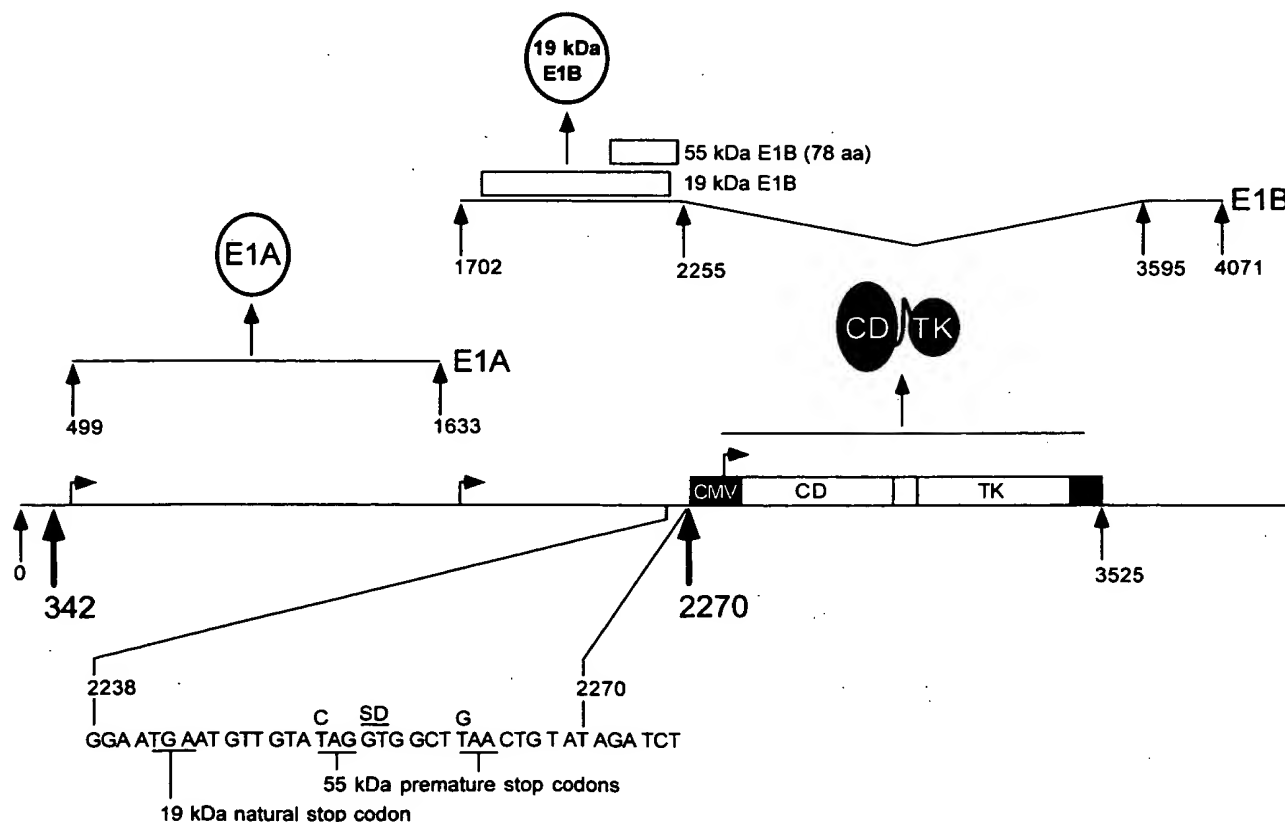


FIG. 1. Schematic representation of the E1 region of FGR. All numbers indicate base positions of the wild-type adenovirus type 5 sequence. The natural 19-kD E1B translation stop codon and the two engineered premature stop codons in the 55-kD E1B reading frame are indicated. Horizontal arrows indicate E1A, E1B, and CMV transcription initiation sites. The caret indicates the intron in the E1B region into which the CD/HSV-1 TK expression cassette was cloned. Solid black boxes in the CD/HSV-1 TK fusion gene represent the CMV promoter or SV40 polyadenylation elements, and the open box indicates the region coding for the polyglycine linker. SD, Splice donor site.

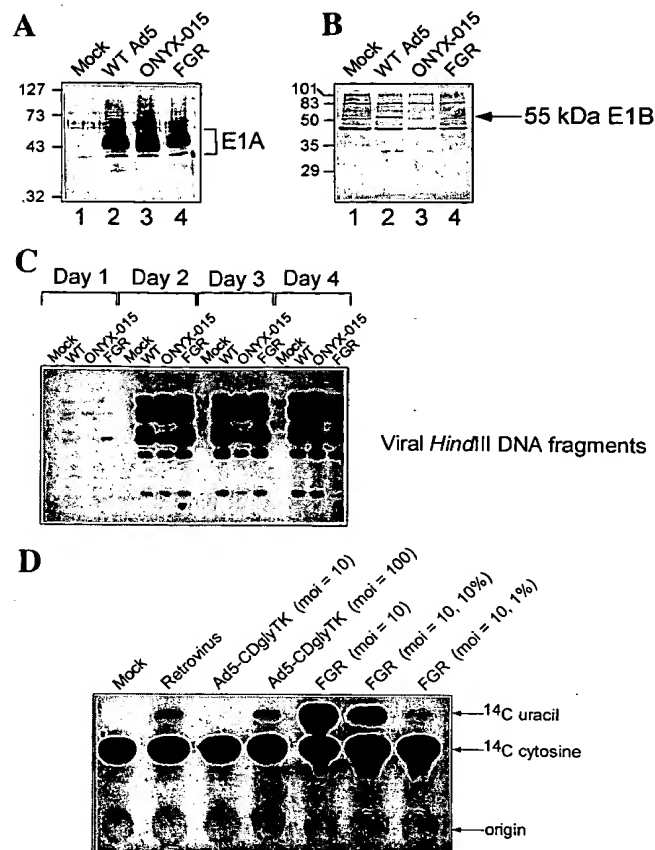


FIG. 2. Characterization of FGR. **A.** Expression of adenovirus E1A proteins. DU145 cells were either mock-infected, or infected with virus at an moi of 10. Cells were harvested 18 hr later and examined for E1A expression by Western blotting. The migration of the E1A proteins is indicated. Numbers on the left indicate molecular weight markers in kilodaltons. **B.** Expression of adenovirus 55-kD E1B protein. DU145 cells were either mock-infected, or infected with virus at an moi of 10. Cells were labeled with [35 S]methionine, and the 55-kD E1B protein was immunoprecipitated from cell extracts. Immunoprecipitates were analyzed on a SDS-10% polyacrylamide gel. The migration of the 55-kD E1B protein is indicated. Numbers on the left indicate molecular weight markers in kilodaltons. **C.** Comparison of viral replication. DU145 cells were either mock-infected or infected with virus at an moi of 10. Cells were harvested every day thereafter, and low-molecular-weight DNA was isolated. DNA was digested with *Hind* III and subjected to Southern blot analysis. The 32 P-labeled probe contained adenovirus type 5 sequences from base 1,340 to the right end and detects all but the left hand-most *Hind* III fragment of the viruses. **D.** Comparison of CD expression among various viruses. DU145 cells were either mock-infected, or infected with FGR at an moi of 10 or a replication-defective version of FGR (Ad5-CDglyTK) at mois of 10 and 100. Cells were harvested 72 hr later and examined for CD activity. All CD assays contained 50 μ g of protein, except for FGR (moi = 10, 10%) and FGR (moi = 10, 1%), which contained 5 μ g and 0.5 μ g, respectively. For comparison, CD expression in adenovirus-infected cells is compared to a pooled, G418-selected DU145 cell line (retrovirus) that expresses the CDglyTK fusion protein from a stably integrated murine provirus (Rogulski *et al.*, 1997a). The [14 C]uracil product and [14 C]cytosine substrate are indicated. The transduction efficiency of DU145 cells at the various mois are as follows: Ad5-CDglyTK, moi = 10, 20–30%; Ad5-CDglyTK, moi = 100, 100%; FGR, moi = 10, 20–30%.

killed tumor cells lacking functional p53, DU145 (human prostate adenocarcinoma, mutant p53), U251 (human glioblastoma, mutant p53), and MRC-5 cells (human diploid fibroblasts, wild-type p53) were infected with graded doses of ONYX-015 and FGR and the resulting cytopathic effect was scored 9 days later (Fig. 3). FGR lysed DU145 and U251 cells with efficiencies identical to ONYX-015. DU145 cells were more sensitive to both viruses than U251 cells. By contrast, both viruses produced only minimal cytopathic effects with MRC-5 cells (at high moi and after prolonged periods). Thus, FGR (and ONYX-015) is able to kill tumor cells containing mutant p53 under conditions where it demonstrates no cytopathic effect on normal cells.

Enhancement of the viral cytopathic effect by the CD/5-FC and HSV-1 TK/GCV suicide gene systems

To determine whether the CD/5-FC and HSV-1 TK/GCV suicide gene systems could enhance the viral cytopathic effect, cells were infected with FGR and exposed to increasing concentrations of 5-FC, GCV, or both 5-FC and GCV. The cytopathic effect was scored qualitatively by staining cells 5–9 days post-infection and quantitatively by clonogenic assays. For U251 cells, both the CD/5-FC and HSV-1 TK/GCV systems increased the cytopathic effect of the virus in a prodrug concentration-dependent manner (Fig. 4A, top). Whereas FGR alone consistently produced about 1 log cell kill in clonogenic assays, 5-FC (≥ 50 μ g/ml) and GCV (≥ 0.5 μ g/ml) each increased the cytotoxic effect by an additional log (Fig. 4B). The effect of FGR on DU145 cells was so potent that it masked the cytopathic effects of the suicide gene systems (not shown). Therefore, we performed similar experiments using another well-characterized human prostate adenocarcinoma cell line, PC-3 (null p53), which is rather resistant to both FGR and ONYX-015. Similar to U251 cells, the CD/5-FC suicide gene system dramatically increased the observed cytopathic effect relative to that of FGR alone (Fig. 4A, middle). However, no increase was observed with the HSV-1 TK/GCV system up to concentrations of 1.0 μ g/ml GCV. Thus, at least one suicide gene system was able to elicit a pronounced cytopathic effect with a tumor cell line that is very resistant to these lytic viruses. Similar results were obtained with the human glioblastoma line LN-Z308 (null p53), which also proved to be resistant to these lytic viruses (not shown). Importantly, when used independently, neither suicide gene system had any significant effect on MRC-5 cells except at the highest (100 μ g/ml) 5-FC concentration used (Fig. 4A, bottom).

CD/5-FC and HSV-1 TK/GCV suicide gene systems markedly inhibit viral replication

Because both the CD/5-FC and HSV-1 TK/GCV systems exert their cytotoxic effect by inhibiting DNA replication either directly (HSV-1 TK/GCV) or indirectly (CD/5-FC), we examined whether these systems could be used to inhibit viral replication. Shortly after FGR infection, cells were plated in increasing concentrations of prodrugs and adenoviral DNA was isolated 2 days later and subjected to Southern blot analysis (Fig. 5). Both suicide gene systems markedly inhibited viral replication. However, in all cell lines tested (U251, DU145, HT29), the HSV-1 TK/GCV system was approximately 1,000-fold more effective on a prodrug concentration basis. This may, in part, be explained

by the fact that the HSV-1 TK/GCV system inhibits DNA replication directly at the level of chain elongation, whereas the CD/5-FC system depletes dTMP precursor pools. Interestingly, a dramatic enhancement of the viral cytopathic effect was observed (Fig. 4A) even at prodrug concentrations that markedly inhibited replication of the virus (for U251 cells: $\geq 50 \mu\text{g/ml}$ 5-FC and $\geq 0.1 \mu\text{g/ml}$ GCV). These results argue that in such cases, the cytopathic effect due to the suicide gene systems is much more potent than that of the virus itself.

Radiosensitization by FGR and prodrugs

Previously, we demonstrated that the CD/5-FC and HSV-1 TK/GCV suicide gene systems could, independently, potentiate the killing effects of radiation *in vitro* (Kim *et al.*, 1994, 1995, 1997; Khil *et al.*, 1996; Rogulski *et al.*, 1997a) and *in vivo* (Rogulski *et al.*, 1997b) (*i.e.*, radiosensitivity). Even greater radiosensitivity was observed when both suicide gene systems were used together (Rogulski *et al.*, 1997a). A tremendous strength of the combined suicide gene therapy/radiotherapy approach is that because neither prodrug (5-FC and GCV) is toxic and it is possible to focus a radiation beam on a very small area in three-dimensional space, it allows for a high degree of tumor cell kill while minimizing damage to normal tissues. Thus, we examined whether these suicide gene systems, when used in the context of a replicating adenovirus, could radiosensitize tumor cells *in vitro*. It is important to note that, because these experiments would employ up to three modalities—viral therapy, suicide gene therapy, and radiotherapy—each of which when used independently under optimal conditions can generate between 1 and 4 logs of cell kill depending on the cell type, it was necessary to use suboptimal amounts of virus and prodrugs to be able to quantify the radiosensitization effect. Thus, the effects described below are likely to represent only a fraction of what could be achieved under optimal conditions.

DU145 and U251 cells were either mock-infected, or infected with FGR at an moi of 1. Two days later, they were exposed to $40 \mu\text{g/ml}$ 5-FC or $0.1 \mu\text{g/ml}$ GCV for 24 hr. Cells then received a single dose of γ -irradiation (0–6 Gy) and were immediately replated for clonogenic assays. Nine days later, colonies were scored and cell survival curves generated. A change in the slope of the cell survival curve relative to radiation alone indicates radiosensitization.

Both the CD/5-FC and HSV-1 TK/GCV suicide gene systems radiosensitized DU145 and U251 cells (Fig. 6A,B), yielding sensitivity enhancement ratios (SERs) in the range of 1.6–3.1. By contrast, FGR alone resulted in no radiosensitization, indicating that the combined toxic effects of the replicating virus and radiation are additive. Thus, even under suboptimal conditions, both suicide gene systems could, in a synergistic manner, enhance the killing effects of radiation when expressed in the context of a replicating adenovirus.

FGR infection of tumors *in vivo*

To estimate the efficiency at which FGR could infect and spread in tumors, HT-29 tumors (human colon adenocarcinoma, mutant p53) were injected with FGR and tumors

were excised and examined for CD expression by immunofluorescence. Although the level of CD expression varied from cell to cell, the results demonstrated that approximately 20–30% of tumor cells expressed the CD gene product (Fig. 7). As expected, the highest CD expression occurred in cells surrounding the injection site. Similar results were obtained with U251 tumors (human glioblastoma, mutant p53; not shown). Thus, it is possible to achieve significant infection of tumor cells *in vivo* using relatively small amounts of the FGR virus.

DISCUSSION

The results presented here demonstrate that suicide gene therapy can enhance the therapeutic effects of viral therapy in a tumor cell-specific manner. The therapeutic effect of these combined modalities can be further enhanced by coupling them with radiotherapy. Although it was not possible to quantify the effectiveness of this three-pronged approach under optimal conditions *in vitro*, it is noteworthy that each modality alone can achieve between 1 and 4 logs of cell kill under optimal conditions depending on the tumor cell type. Thus, even if the combined cytotoxic effects of these modalities was simply additive under optimal conditions, it should be possible to achieve very significant cell kill when these three modalities are used simultaneously. That suicide gene therapy and radiotherapy interact to produce a synergistic enhancement of cell kill may make the combined therapeutic effect even greater. Thus, the three-pronged approach described here (Fig. 8) may prove to be a very powerful means of destroying cancer cells *in vivo*.

Despite its potential, however, improving the effectiveness of a treatment is of no clinical value if there is no significant increase in the therapeutic index, the differential response between tumor and normal tissue. When taking this important point into consideration, the three-pronged approach described here fares well. As demonstrated previously (Bischoff *et al.*, 1996; Heise *et al.*, 1997) and here, the use of an E1B-attenuated adenovirus allows for the preferential targeting of tumor cells lacking functional p53. Thus, the viral cytopathic effect, although not restricted to tumor cells lacking functional p53, is preferentially observed in such cells relative to normal cells. Although the suicide gene systems do not specifically target tumor cells, they do target replicating cells and, importantly, unlike conventional chemotherapy, neither prodrug produces significant systemic toxicity in humans. Finally, with three-dimensional conformal radiotherapy, it is possible to deliver high doses of radiation specifically to a tumor site while minimizing the exposure to surrounding tissues. On the basis of these premises, we believe the three-pronged approach described here may generate a significant increase in the therapeutic index when used in the clinic.

Nearly all gene therapy protocols undergoing clinical trials today are limited by low *in vivo* gene transduction efficiencies. Although several approaches using replication-defective retroviruses or adenoviruses have produced encouraging results in animal models, it is unlikely that these approaches will have the gene transduction efficiencies necessary for them to be ef-

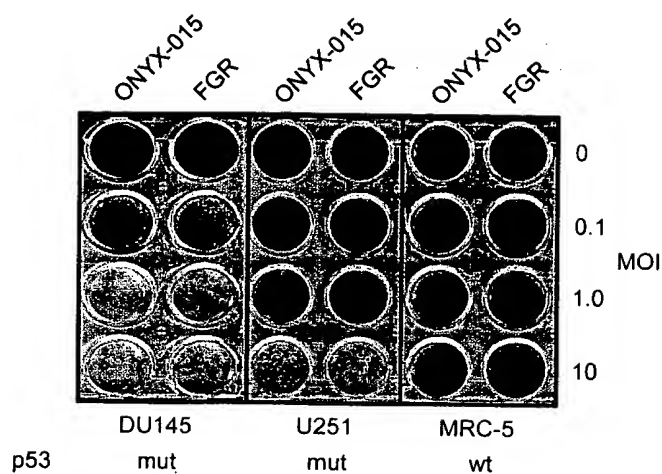


FIG. 3. Comparison of ONYX-015 and FGR cytopathic effects. Cells were either mock-infected (moi = 0), or infected with virus at the mois indicated. Cells were fixed and stained with crystal violet 9 days later.

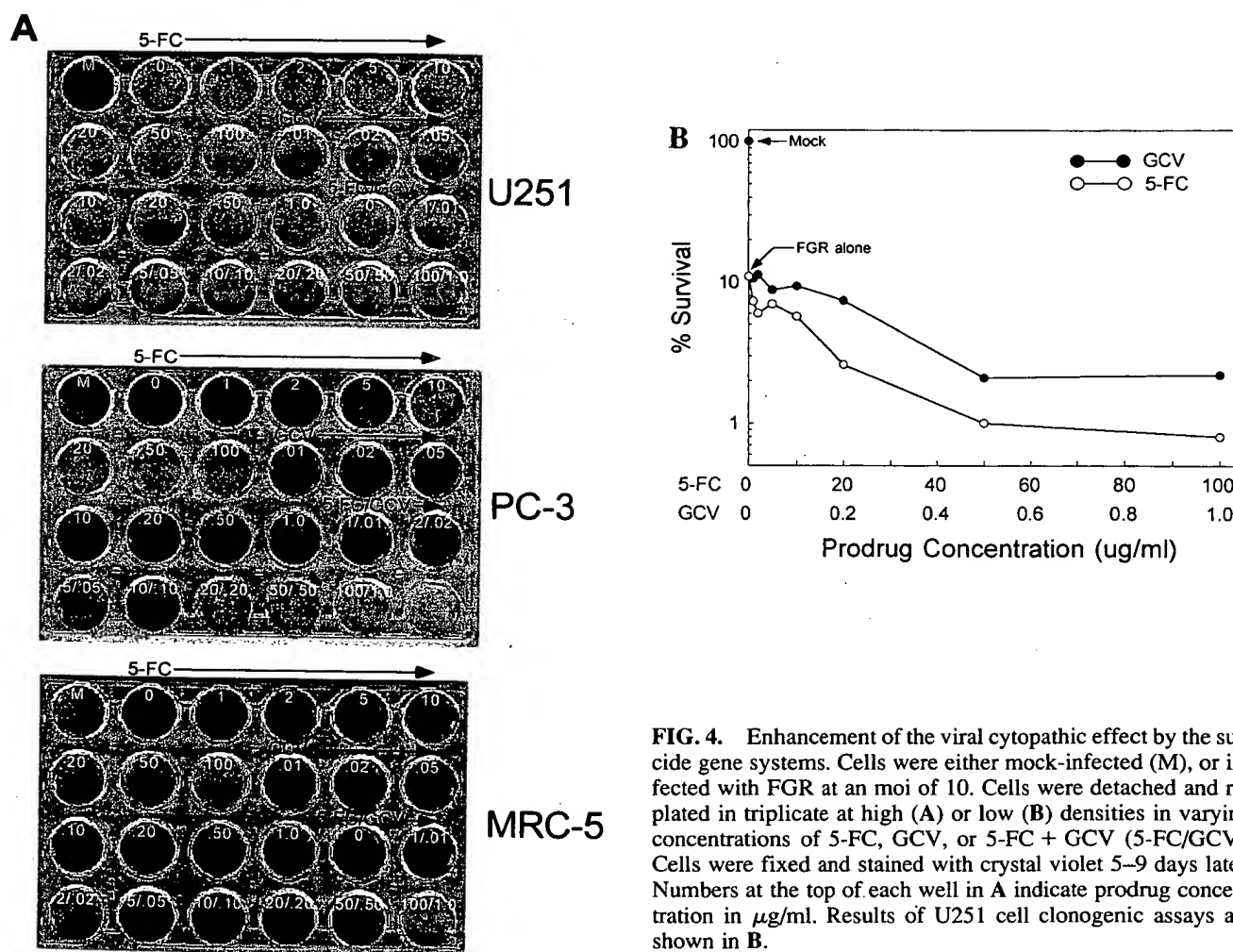


FIG. 4. Enhancement of the viral cytopathic effect by the suicide gene systems. Cells were either mock-infected (M), or infected with FGR at an moi of 10. Cells were detached and replated in triplicate at high (A) or low (B) densities in varying concentrations of 5-FU, GCV, or 5-FU + GCV (5-FU/GCV). Cells were fixed and stained with crystal violet 5–9 days later. Numbers at the top of each well in A indicate prodrug concentration in $\mu\text{g/ml}$. Results of U251 cell clonogenic assays are shown in B.

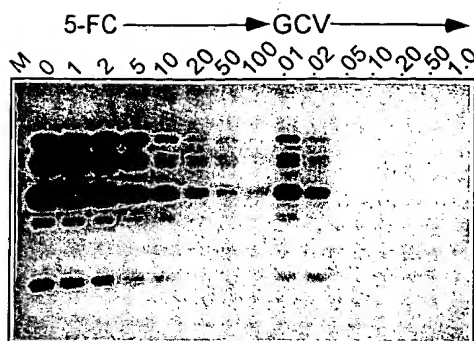
Viral *Hind*III DNA fragments

FIG. 5. Inhibition of virus replication by suicide gene systems. Cells were either mock-infected (M), or infected with FGR at an moi of 10. Cells were detached and replated in varying concentrations of prodrugs. Cells were harvested 48 hr later for isolation of low-molecular-weight DNA. DNA was digested with *Hind* III and analyzed by Southern blotting as described in Fig. 2C.

fective against the large tumoral masses commonly observed in human cancer patients. Moreover, because few human cancers are curable with a single modality, it has been our tenet that the promise of cancer gene therapy will be realized only when used in combination with other modalities, such as the ones described here. We believe the three-pronged approach described here may improve not only the specificity (discussed above), but also the efficacy, of the cancer gene therapy approach. Relative to a replication-defective virus, the replication capacity of FGR should result in a markedly greater efficiency of gene transfer *in vivo* as well as higher transgene expression per tumor cell. Indeed, we have observed that FGR is able to produce up to

2,000-fold more CD activity in infected cells than a replication-defective version from which FGR was derived (after correcting for differences in mois). This should result in a greater therapeutic effect per dose than that obtainable with replication-defective viruses. It is possible that the high *in vivo* gene transduction efficiencies observed with replication-competent adenoviruses may enable this approach to be efficacious against disseminated disease (Heise *et al.*, 1997).

Another potential strength of the approach described here is that both suicide gene systems proved to be effective at inhibiting viral replication *in vitro* at prodrug concentrations that are safely achievable in humans. Although it is uncertain

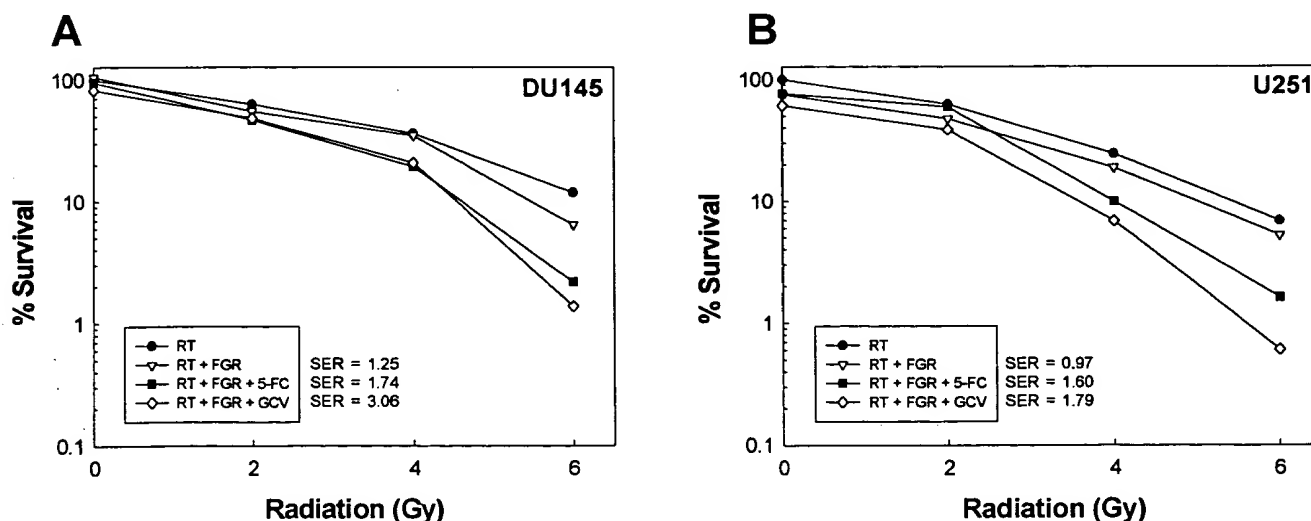


FIG. 6. Radiosensitization by the suicide gene systems. DU145 (A) and U251 (B) cells were either mock-infected (●), or infected with FGR at a moi of 1. Forty-eight hours later, cells were incubated in growth medium without (▽), or with, prodrugs at 40 μ g/ml 5-FC (■) or 0.1 μ g/ml GCV (◇) for 24 hr. Cells were then exposed to a single dose of γ -irradiation (0–6 Gy) and replated in triplicate for clonogenic assays. Colonies were fixed, stained with crystal violet, and counted 7–10 days later. The SER represents the ratio between the D_0 of radiation alone (RT) and the D_0 for radiation plus FGR without (RT + FGR), or with (RT + FGR + 5-FC, RT + FGR + GCV), prodrugs. The radiosensitization experiments were performed twice and the SERs varied less than 10% between experiments.

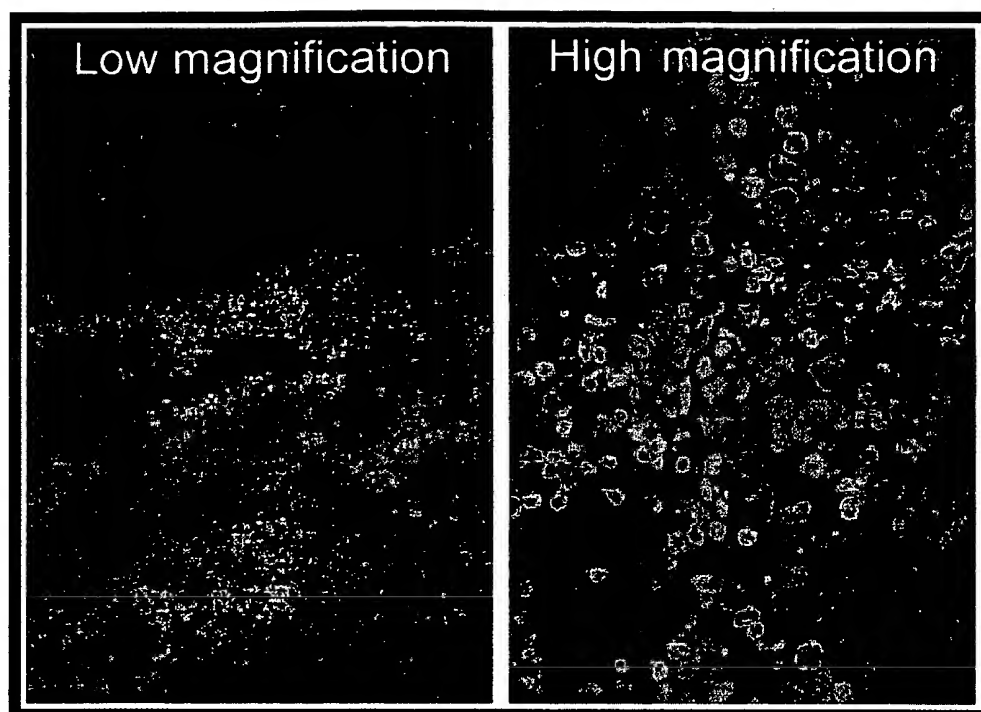


FIG. 7. FGR infection of tumor cells *in vivo*. HT-29 tumors (0.2 cm^3) were injected with 10^8 pfu ($50 \mu\text{l}$) of FGR on 5 consecutive days. Two days after the last injection, tumors were excised, sectioned, and processed for immunofluorescence. Samples were photographed at a magnification of $25\times$ (left) and $125\times$ (right). Cells that are positive for CD expression appear red. Nuclei were stained with DAPI and are blue.

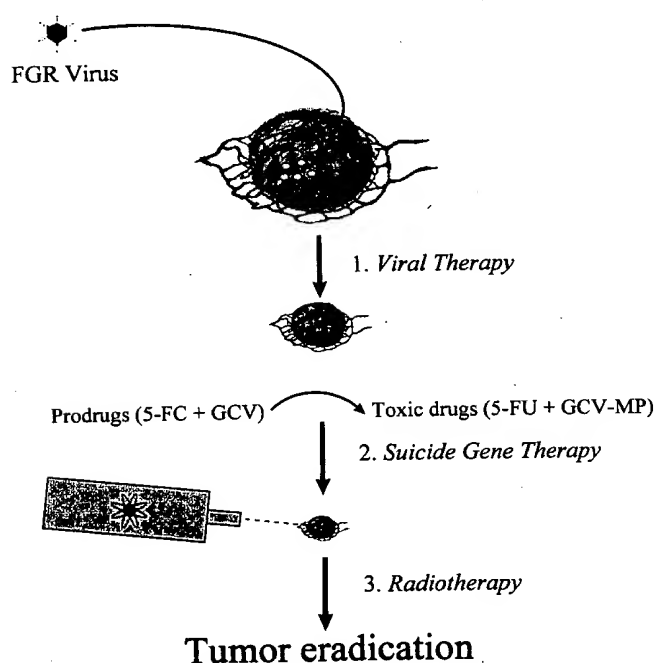


FIG. 8. Schematic diagram of three-pronged approach. The FGR virus itself (prong 1) replicates in and preferentially kills tumor cells expressing mutant p53 resulting in significant, and selective, tumor cell destruction. Co-utilization of the CD/5-FC and HSV-1 TK/GCV suicide gene systems (prong 2) markedly enhance the therapeutic effects of the FGR virus and, importantly, sensitize tumors to radiation (prong 3). The replication potential of the FGR virus enhances both the efficiency of gene transduction (percentage of tumor cells (infected) as well as the steady-state level of transgene expression per cell.

whether uncontrolled viral spread will prove to be a drawback of this approach, having the potential to eliminate the virus, if necessary, is an asset. These observations also make it likely that following injection of the virus, both the timing and dose of prodrug administration will be critical parameters in determining the therapeutic outcome. Indeed, results from our ongoing animal studies support this notion. Thus, inclusion of the CD/HSV-1 TK fusion gene in a lytic, replication-competent adenovirus may not only improve the efficacy, but also the safety, of this cancer gene therapy approach.

There is perhaps one additional advantage of the three-pronged approach described here. Although the use of an E1B-attenuated adenovirus, such as ONYX-015, allows for the preferential destruction of tumor cells lacking functional p53, its inability to destroy tumor cells selectively with normal p53 is a weakness. Moreover, we have observed that some human tumor cell lines are resistant to these lytic viruses. These weaknesses may prove to be significant as many human tumors show intratumoral heterogeneity with respect to p53 status (Mirchandani *et al.*, 1995; Yang *et al.*, 1996) and the efficacy of this approach may vary widely among tumor types. Thus, a better approach might be one that could selectively destroy tumor cells lacking, or containing, functional p53, and yet inflict minimal damage on surrounding normal cells. Indeed, FGR, when used in conjunction with prodrug and radiation therapy, may meet such criteria. It has been previously demonstrated that tumor cells with normal p53 status are more sensitive to the cytotoxic effects of chemotherapeutic drugs, such as 5-FU, and radiation than tumor cells lacking functional p53 (Lowe *et al.*, 1993, 1994). The heightened sensitivity of tumor cells with normal p53 is thought to be due to their increased propensity to undergo p53-mediated apoptosis following injury.

Because our three-pronged approach employs both chemotherapy and radiotherapy, it is possible that FGR, when combined with these modalities, may selectively destroy both tumor cell types. Whereas the viral cytopathic effect should selectively target tumor cells lacking functional p53, the suicide gene systems, via their bystander effects, and radiotherapy should preferentially target those containing functional p53. Importantly, this approach should inflict minimal damage on surrounding normal cells because such cells are less likely to be replicating (and therefore resistant to suicide gene therapies) and normal cells tend to undergo p53-mediated growth arrest, not apoptosis, following insult by chemotherapeutic drugs and/or radiation (Lowe *et al.*, 1993). Thus, utilization of the suicide gene systems should not significantly weaken the specificity of the "tumor-specific" E1B-attenuated adenoviruses. We have already demonstrated that FGR, in conjunction with 5-FC prodrug therapy, is able to kill effectively tumor cells that are resistant to lytic viruses such as ONYX-015 and FGR.

Thus, it is likely that the three-pronged approach described here will prove to be a significant improvement over ONYX-015 because the three modalities may target different tumor cell types or subpopulations, which, in turn, should expand the spectrum of human tumors that it will be effective against. Indeed, our ongoing studies in animals have confirmed that the addition of double suicide gene therapy significantly improves the antitumor effects (*i.e.*, tumor growth delay and tumor cure) of E1B-attenuated, replication-competent adenoviruses.

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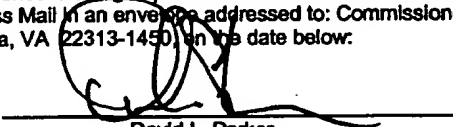
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Address reprint requests to:
Dr. Svend O. Freytag
Molecular Biology Research
Henry Ford Health System
One Ford Place, Wing 5D
Detroit, MI 48202-3450

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CERTIFICATE OF MAILING 37 C.F.R. 1.8	
I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail in an envelope addressed to: Commissioner for Patents, P. O. Box 1450, Alexandria, VA 22313-1450, on the date below:	
12/3/03 November 12, 2003 Date	 David L. Parker

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:
Wold *et al.*

Serial No.: 09/351,778

Filed: July 12, 1999

For: Replication Competent Anti-Cancer Vectors

Group Art Unit: 1632

Examiner: Priebe, Scott David

Atty. Dkt. No.: 66153-7775

SUPPLEMENTAL DECLARATION OF THE INVENTORS UNDER 37 C.F.R §1.131

We, William S.M. Wold, Ann E. Tollefson, Konstantin Doronin and Karoly Toth, declare as follows:

1. We are joint inventors of the subject matter claimed in the referenced patent application. We are submitting the present §131 declaration to supplement our earlier declaration filed January 6, 2003, the contents of which are incorporated herein by reference.
2. In our earlier declaration we demonstrated that the adenovirus vector KD1 was constructed prior to March 3, 1997, and, in numerous studies that we conducted between 5/9/97 and 6/2/97, KD1 was shown to overexpress ADP. We are submitting the present Supplemental Declaration to supplement our earlier declarations by demonstrating that (1) prior to March 3, 1997, we conceived of using ADP-expressing adenoviral vectors for treating cancer in patients,

and that (2) shortly after March 3, 1997 an exemplary vector, KD1, was tested in an animal having cancer and shown to have anticancer activity.

3. Prior to March 3, 1997 we conceived of the idea of using adenovirus vectors expressing the ADP gene as a therapeutic agent to treat cancer. This is shown, for example, in the exhibits to our 1/6/03 declaration, in particular, Exhibit B at, for example, page 3, section B, and pages 4-8. The Exhibit B document is dated prior to March 3, 1997.

4. On July 7, 1997, we sent KD1, dl1101/1107, dl309, and A549 cells to Dr. Jeffrey A. Whitsett at the Children's Hospital Medical Center, Division of Pulmonary Biology, Cincinnati, OH. A copy of the cover letter sent to Dr. Whitsett is attached as Exhibit M. Dr. Whitsett had agreed to test these vectors on our behalf in the A549 nude mouse model, in which A549 human lung carcinoma cells are used to establish tumors in nude mice following by injection of the various vectors to determine their anticancer efficacy. On September 16, 1997, we received a report from Dr. Whitsett's colleague, Lee Zhang, indicating that "10⁹ pfu of each of the viruses were injected into each established A549 tumor. 4 out of 6 tumors injected with KD1 showed slowed tumor growth while 2 out of 2 tumors injected with dl309 and 4 out of 4 injected with dl 1101/1107 continued to grow." A copy of this fax is attached as Exhibit N.

5. Accordingly, foregoing studies conducted on our behalf demonstrated the successful use of KD1 in the treatment of cancer in an animal at least as early as September, 1997.

6. We hereby declare that all statements made of our own knowledge are true and all statements made on information are believed to be true and further that the statements were made with the knowledge that willful false statements and the like so made are punishable by fine or

imprisonment or both under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issued thereon.

December 1, 2003
Date

William S.M. Wold
William S.M. Wold

December 1, 2003
Date

Ann E. Tollefson
Ann E. Tollefson

December 1, 2003
Date

Konstantin Doronin
Konstantin Doronin

December 1, 2003
Date

Karoly Toth
Karoly Toth

7/8/97

Dear Jeff:

- Please find enclosed:

dl309, 2.15×10^8 PFU/ml, ~ 200 μ l

dl1101/1107, 1.95×10^8 PFU/ml, 2 ml

KD1, 9×10^{10} PFU/ml, 2 ml

A549 cells, passage 78.

- dl309 is Ad5, with the E3 10.4K, 14.5K, 14.7K genes ^{deleted}
- dl1101/1107, deletes the RB and p300 binding sites required to drive cells from G₀ \rightarrow S phase, in dl309 ^{background}
- KD1, is in dl1101/1107 background.
Lacks all E3 (stealth) genes. Engineered to overexpress the Adenovirus Death Protein (ADP).

- Bill

FAX MESSAGE

DATE 9/16/97

TO

Name Bill Wald

Address _____

Fax Number 314 713 3403 Phone Number _____

Number of pages (including this one): 1

MESSAGE: 10⁷ pfu of adenovirus were injected into each
established R49 tumor. 4 out of 6 tumors injected
with KD1 showed slowed tumor growth while 2 out of
2 tumors injected with dl 309 and 4 out of 4 injected
with dl uet/uet continued to grow.

FROM

Name Lee Zhang

CHILDREN'S HOSPITAL MEDICAL CENTER

DIVISION OF NEONATOLOGY

3333 Burnet Avenue

Cincinnati, Ohio 45229-3039

Phone (513) 636-7992

Fax (513) 636-7888

EXHIBIT

A1

FRO

ITY MMI

FAX NO. : 3147733403

Dec. 19 2002 10:21AM P2

Time Counted			87/972 plaque assay
			(Cumulative)
1041	801		
106	19 88	37 120	DME
2 83	20 108	38 114	55 0
3 84	21 95	39 123	56 0
			57 (all cells dead)
4 13	22 14	40 16	Ad5 → distinct plga 1035 → not as definitive 1038 →
5 12	23 14	41 12	
6 5	24 12	42 12	
1035 7 omit → cells dead	918 25 78	716 43 1	1041 → more distinct plga
8 69	26 74	44 1	918 → distinct
9 68	27 71	45 1	305 → distinct
10 11	28 14	46 0	Large plaques 716 → largest, most distinct plaques
11 9	29 8	47 1	
12 9	30 10	48 0	
1038 13 110	305 31 41	712 49 46	Small plaques 801 → very small + slow growth 712 → very small with slow growth
14 107	32 37	50 57	
15 85 (but high cell death)	33 41	51 52	
16 16	34 5	52 (total cell death)	
17 7	35 1	53 6	
18 9	36 6	54 8	

10 SHEETS 3 SQUARE
20 SHEETS 3 SQUARE
30 SHEETS 3 SQUARE
40 SHEETS 3 SQUARE
50 SHEETS 3 SQUARE
60 SHEETS 3 SQUARE
70 SHEETS 3 SQUARE
80 SHEETS 3 SQUARE
90 SHEETS 3 SQUARE
100 SHEETS 3 SQUARE

A2

11.6K → possibly related to plaque size
 + morphology?
 (tend to vary more
 in plaque size)

Plaque SizeLarge & distinct

dl 753 (esp.)

dl 754

dl 714

dl 778

Ad 5 (esp.)

dl 799

~~dl 778~~

dl 716 (esp.)

dl 751 (esp.)

dl 718

Smaller / less distinct

most SPY 10.4K mutant

[pa 775 more distinct + larger]

pm 771

dl 713

dl 327 (smaller than
rec 700 in dl 728)Small

748

712

dl 801

dl 766

dl 742

pm 785

In 724

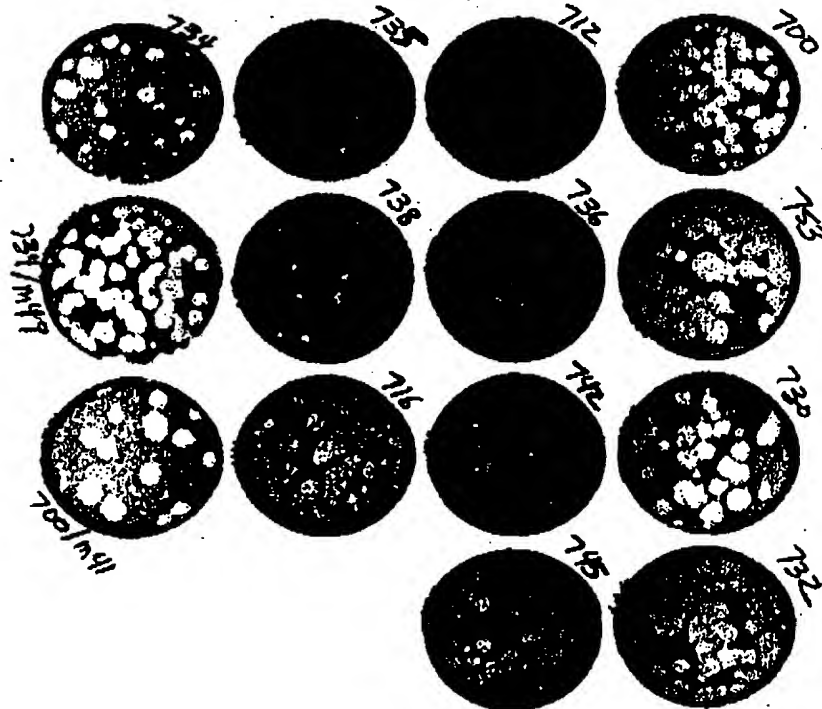
dl 748

dl 706

dl 708

dl 717

dl 7001

E3-11.6k Small Plaque Mutants

Early work
on defining
ADP function

EXHIBIT**A3**

EXHIBIT

A4

Plaque Assays

(11.6K Mutants ^{to test} ~~plaque assay~~)

11 P.A. dishes

 5×10^9 5×10^{10}

Virus	Prep	Titre	5×10^9	5×10^{10}
① rec 700 (VS188) (910515)		2.37×10^{11}	2	3
② dl 742 (860313)		1.77×10^{11}	2	3
③ dl 745 (860313)		2.06×10^{11}	2	3
④ dl 712 (ply 1) (VS204) (911101)		1.56×10^{11}	2	3
⑤ dl 730 (39-4) (VS168) (901214)		1.73×10^{11}	2	3
⑥ dl 732 (2 ^{1/2}) (AS) (890414)		3.4×10^{11}	2	3
⑦ pm 734 (1 ^{1/2}) (890504)		6.7×10^{10}	3	2
⑧ dl 735 (3 ^{1/2}) (890425)		$9. \times 10^{10}$	3	2
⑨ dl 736 (0.0 ^{1/2}) (890414)		2.88×10^{10}	3	2
⑩ dl 738 (38-11) (VS171) (910118)		?	3	3
⑪ 700/m41 (AS) (920214)		?	3	3
⑫ pm 734/m49 (AS) (920402)		?	3	3
⑬ dl 716 (ply. 4) (VS125) (900202)		2.04×10^{11}	1	2
⑭ dl 753 (VS78) (880624)		1.42×10^{11}	1	2
⑮ mock		-	(150)	

SF-DME for all pre-infection;
infection with 0.5 ml of dilutions at 4:30 pm;
added 6 ml of overlay at 5:45 pm;

(5/29) added 5 ml of NR overlay; one dish of
dl 738 (0.5×10^9 dilution) dropped → discarded

on (5/29) see large distinct plaques on dl 730, dl 732,
dl 716, dl 753 dishes (+ some dl 715), rec 700 may
have a few smaller plaques & really do not
see plaques on other dishes yet.

EXHIBIT

AS

(1/2) plaques were visible
(6/3) marked in green

Counts of (1/25) Plaque Assays

Sample	Dilution	A	B	C	Comments
① rec 700 (V5188)(910503)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+39 55 +8 2	+35 51 +4 2	- +4 3	quite large & distinct vary in size. how distinct (similar to rec 730, 732, 733)
② dl 742 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+23 0 0	+52 +1 0	- 0 0	very indistinct very tiny & indistinct
③ dl 745 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+20 24 +2 5	+13 22 +1 1	- +2 3	quite large & ^{slightly} darker quite distinct Similar size to rec 700
④ dl 712 (ply 1) (V5204)(911100)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+8 0 +1 0	+6 0 0 0	- 0 0	no plqs. visible. (at least not definitive) very small plaques
⑤ dl 730 (39-4) (V5168)(901214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+16 20 +1 1	+22 20 +4 3	- +1 7	quite large & ^{probably} larger than distinct rec 700
⑥ dl 732 (29/1) (AS)(890414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+8 72 +3 4	+12 52 +3 1	- +3 5	larger & more distinct than dl 730 & dl 733 larger & very distinct
⑦ pm 734 (19/2) (870504)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+16 4 +4 0	+8 1 +2 0	+20 5 -	probably not very small, but very indistinct ^{prob. smaller} than rec 700
⑧ dl 735 (39/1) (890425)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+8 6 0 0	+1 0 +1 0	(+13 5) - -	indistinct plaques, size not very definite very small & indistinct
⑨ dl 736 (00/1) (870414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+1 1 0 0	+2 1 0 0	+4 1 -	indistinct plaques very small & indistinct

EXHIBIT

A6

(7/3) plaques

(9/3) marked in green

Counts of (5/25) Plaque Assays

Sample	Dilution	A	B	C	Comments
(10) dl738(38-11) (V5171)(710118)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+6 4 0 0	+1 11 0 0	— 0 0	not too small, but not very distinct small & indistinct
(11) 700/m41 (ASX920214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+7 8 +0 2	+3 11 +2 0	+12 10 +1 2	~ like rec 700 quite large & very distinct
(12) pm 734/m49 (AS) (920402)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+35 28 +11 3	+13 31 +6 4	+46 36 +7 1	~ like rec 700 ~ like rec 700
(13) dl716(plg4) (V5125)(700202)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+26 62 +1 5	— +1 3	— —	quite large & distinct larger & more distinct than rec 700
(14) dl753 (V5178)(880624)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+13 42 +2 2	— +0 3	— —	quite large & distinct very large & distinct
(15) mock	—	0 0	—	—	good monolayer

EXHIBIT

A7

Counts of (75) Plaque Assays

Sample	Dilution	A	B	C	Comments
① rec 700 (V5188)(910503)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+13 +0	+16 +3	- +1	plaques quite large distinct, new plaques distinct
② dl 712 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+6 0	+5 +1	- 0	new plaques very indistinct, older plaques still small with diffuse edges
③ dl 745 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+7 +2	+7 +0	- +1	large, distinct plaques; new plaques very distinct
④ dl 712 (plg1) (V5204)(911101)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+6 +0	+10 0	- 0	small + indistinct older plqs still small
⑤ dl 730 (39-4) (V5168)(901214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+6 +1	+8 +1	- +2	very large to very distinct plaque new plqs distinct
⑥ dl 732 (29) (A5)(890414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+4 +0	+2 +4	- +1	Very large + distinct plaque
⑦ pm 734 (19/2) (890504)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+19 +2	+17 +1	+13 -	plaques a bit smaller than rec 700; new plaque quite distinct
⑧ dl 735 (34/1) (890425)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+6 +1	+12 +1	+13 -	small + very indistinct plaq
⑨ dl 736 (0.04/1) (890414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+5 +1	+5 0	+6 -	very small + very indistinct (both old + new)

(1/2) max (1/2) min

EXHIBIT

A8

Counts of (5/25) Plaque Assays

Sample	Dilution	A	B	C	Comments
(10) dl 738 (38-11) (V5171)(910118)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+5 +1	+6 0	— 0	new plaques very small & indistinct, even older plaques are ~ 0 size with diffuse edges
(11) 700/m41 (AS)(920214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+5 +0	+2 +0	+5 +0	plaques large, new plaques very distinct (similar size to much older 738)
(12) pm 734/m49(AS) (920402)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+17 +4	+16 +1	+17 +5	new plaques very distinct, fairly large & distinct, maybe a bit smaller than vac 700 plaque
(13) dl 716 (plg 4) (V5125)(900202)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+1 +1	— +1	— —	very large & distinct (exp. on 10^{-10})
(14) dl 753 (V578)(880624)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+7 +1	— +2	— —	very large & distinct
(15) mock	—	0	—	—	good monolayer

EXHIBIT

A9

Counts of (FCs) Plaque Assays

Sample	Dilution	A	B	C	Comments
① rec 700 (V5138)(910503)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+3 +1	+6 +1	- +1	distinct fairly large plaques
② dl 742 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+20 +3	+22 +2	- +1	small & indistin. plaques; new plaques "pinpoint"
③ dl 745 (860313)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+7 +0	+2 +0	- +1	large distinct plaques
④ dl 712 (plg 1) (V5204)(911101)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+28 +1	+29 +1	- +2	very small plga; new plga "pinpoint"
⑤ dl 730 (39-4) (V5168)(901214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+1 +1 (mild)	+4 +0	- +0	very large, nice plaques (edges a bit diffus)
⑥ dl 732 (29/1) (A5)(890414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+7 +0	+1 +0 (mild)	- +1	very large, nice plaques
⑦ pm 734 (1 1/2) (890504)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+28 +2	+28 +3	+25 -	slightly small plaques, new plaques fairly big & distinct
⑧ dl 735 (3 1/1) (890425)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+18 +5	+34 +7	+30 -	older plga times new plga - "pinpoints"
⑨ dl 736 (0.04/1) (890414)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+11 +0	+22 +0	+15 -	very small plga new plga "pinpoints"

EXHIBIT

A10

(10) marked in black

Counts of (5/25) plaque Assays

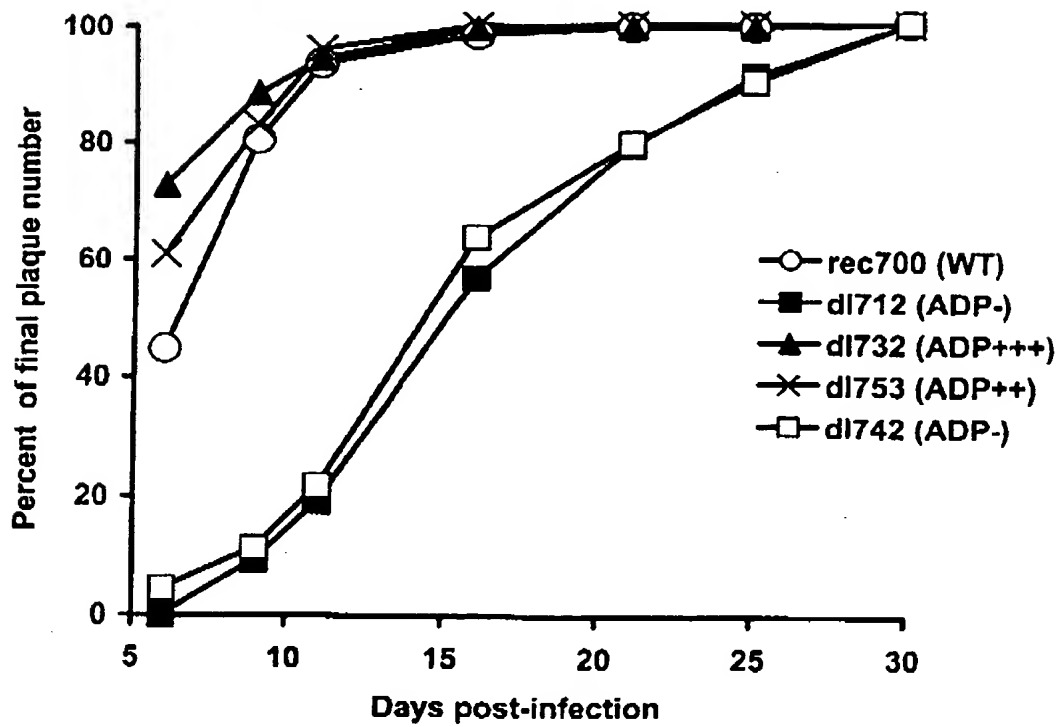
Sample	Dilution	A	B	C	Comments
(10) dl 738 (38-11) (VS171)(910118)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+22 +2	+16 +3	- +3	small + indistinct, new plaques very small
(11) 700/m41 (AS)(920214)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+3 +1	+5 +0	+4 mm +0	new plqs larger than oldest of dl 738; large plaques + distinct
(12) pm 734/m49(AS) (920402)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+5 +2	+7 +3	+15 mm +4	large distinct plaques (new plqs larger than oldest (738))
(13) dl 716 (ply 4) (VS125)(900202)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+3 +1	- +1	- -	very large + distinct
(14) dl 753 (VS 78)(880624)	$.5 \times 10^{-9}$ $.5 \times 10^{-10}$	+1 +0	- +2	- -	very large + distinct
(15) mock	-	0	-	-	good monolayer

EXHIBIT

All

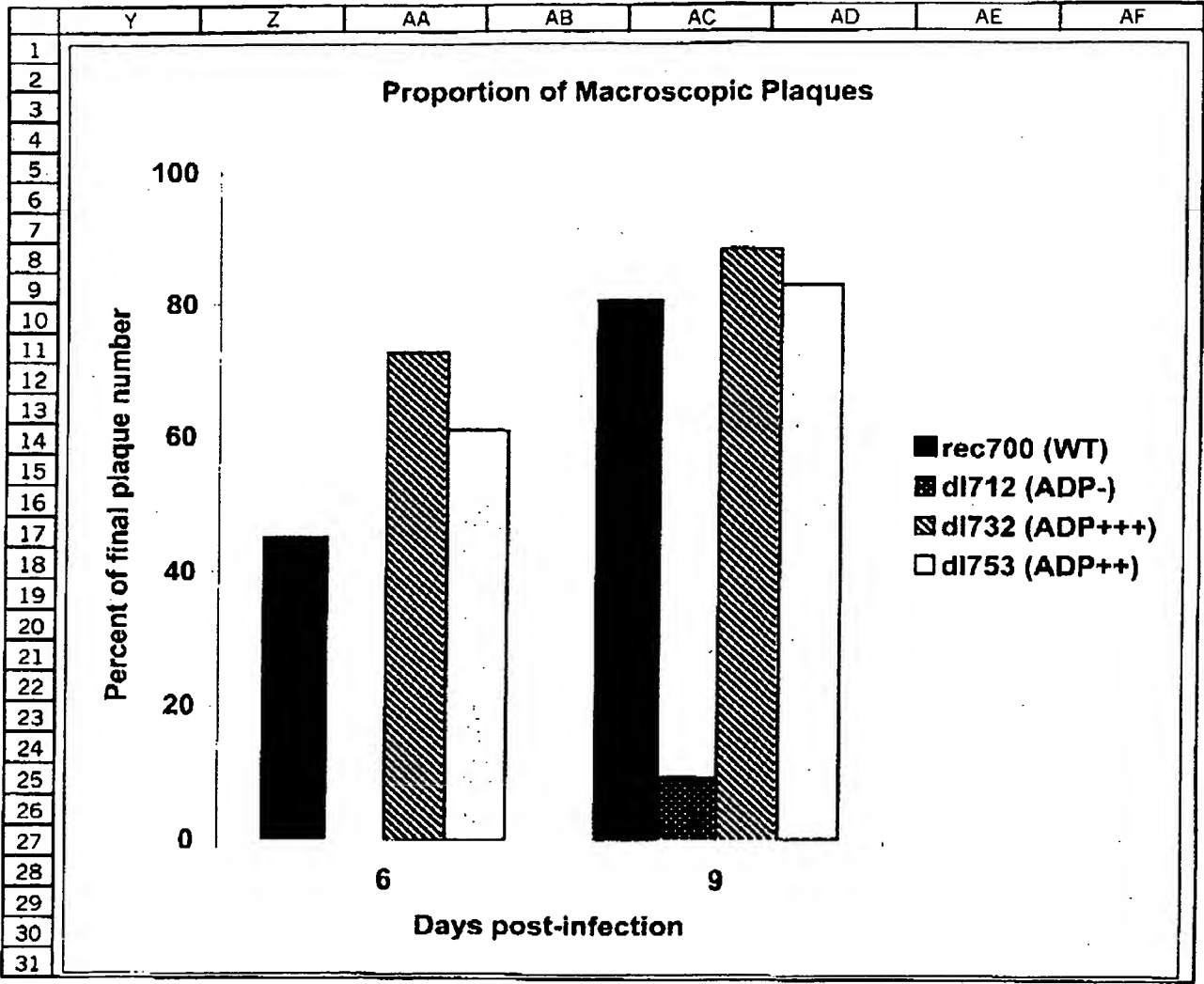
5/25/03

plaque assay



EXHIBIT

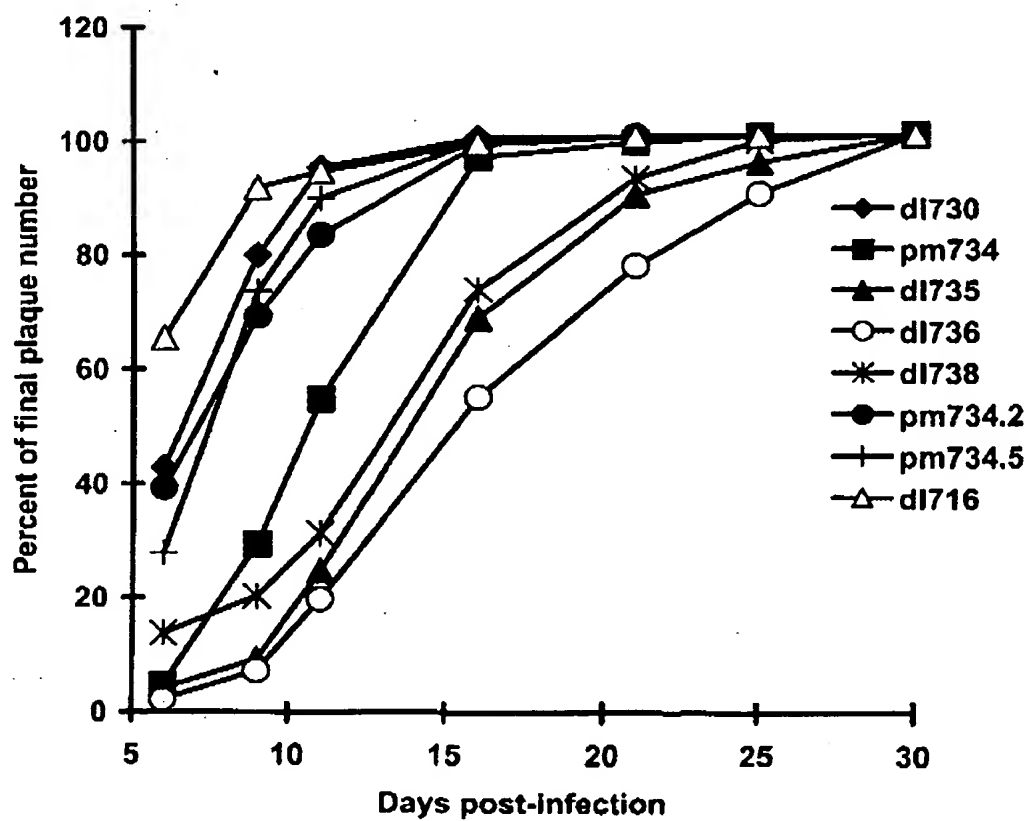
A12



A13

00382

Plaque assay



EXHIBIT

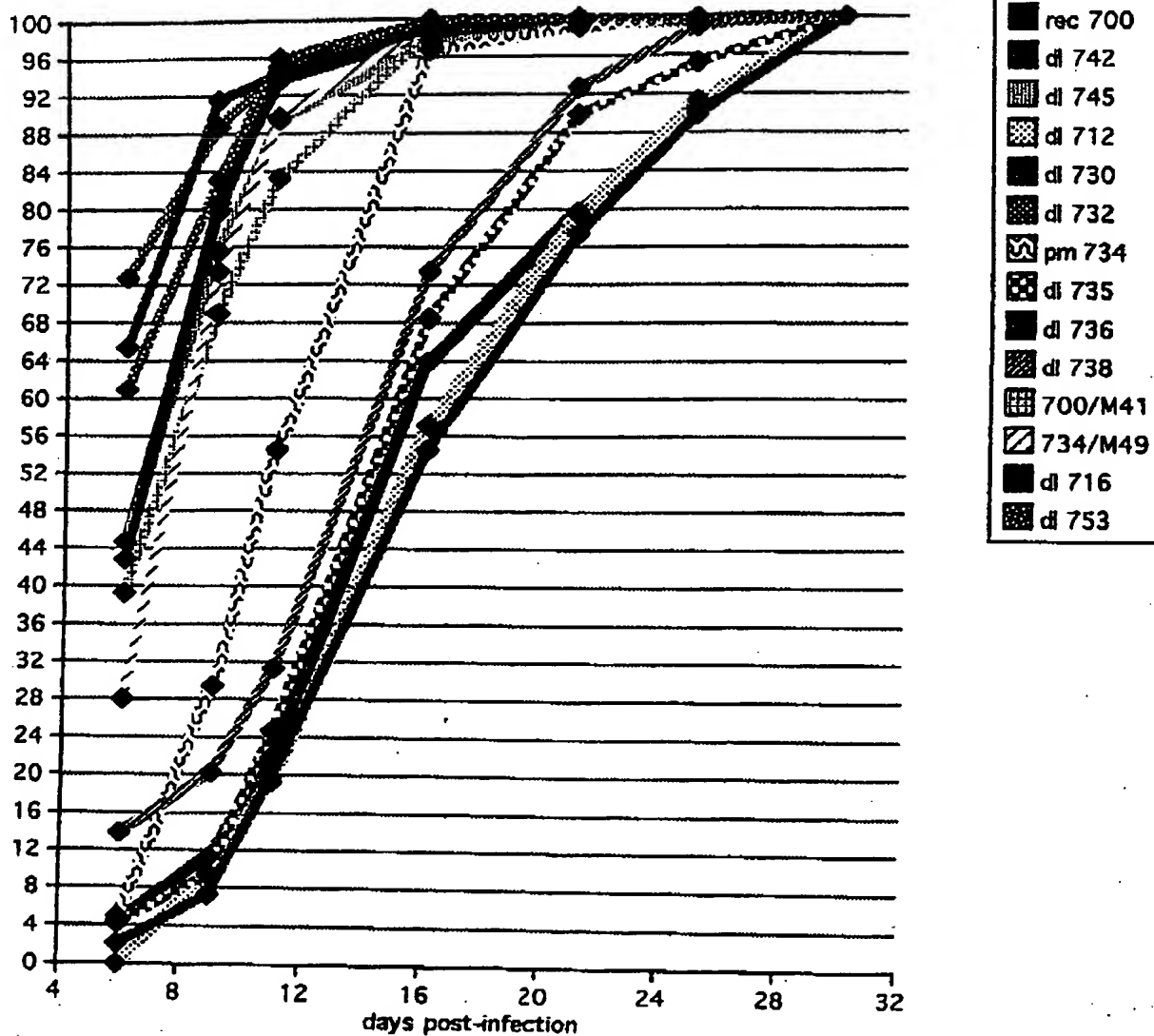
A14

	B	C	D	E	F	G	H
2	6	9	11	16	21	25	30
3	rec700 (WT)	44.8	80.6	93.7	98.4	99.6	100
4	dl712 (ADP-)	0	9.3	19.3	57.1	79.5	100
5	dl732 (ADP+++)	72.8	88.6	94.6	99.5	99.5	100
6	dl753 (ADP++)	61	83.1	96.1	100	100	100
7	dl742	4.4	11.4	21.9	64	79.8	100
8	dl745	44.7	75.6	89.4	97.6	99.2	100
9	6	9	11	16	21	25	30
10	dl730	42.9	79.8	95.1	100	100	100
11	pm734	4.9	29.3	54.6	96.6	99	100
12	dl735	4.2	9.3	24.7	68.4	89.8	100
13	dl736	2.2	7.3	19.7	54.7	77.4	100
14	dl738	13.8	20.2	31.2	73.4	92.7	100
15	pm734.2	39.3	69	83.3	98.8	100	100
16	pm734.5	27.9	73.4	89.7	99.5	100	100
17	dl716	65.4	91.6	94.4	99.1	100	100
18							
19							
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22							
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24							
25							
26							
27							
28							
29							
30							
31							

EXHIBIT

ALS

Plaque Assays



A-16

D. :3147733403

[illegible]

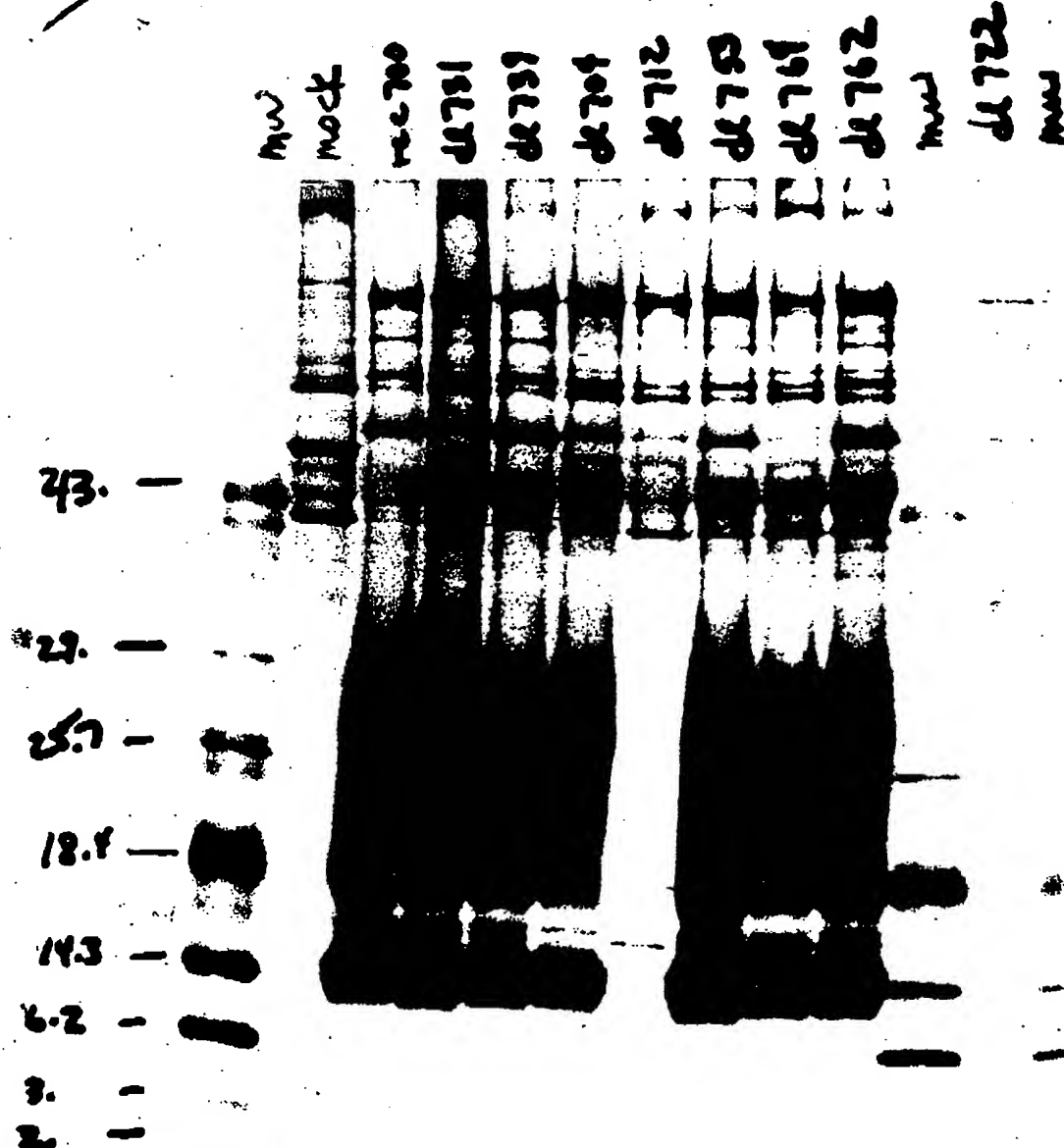
FAX NO. : 314

A17

19 2002 10:30AM P16

Y.A. (p. 2)

[illegible]



EXHIBIT

A18

Gel #1

13 day exposure

5 min developer

709 #1

11.6 (Deletion Mutation)

8/9 →

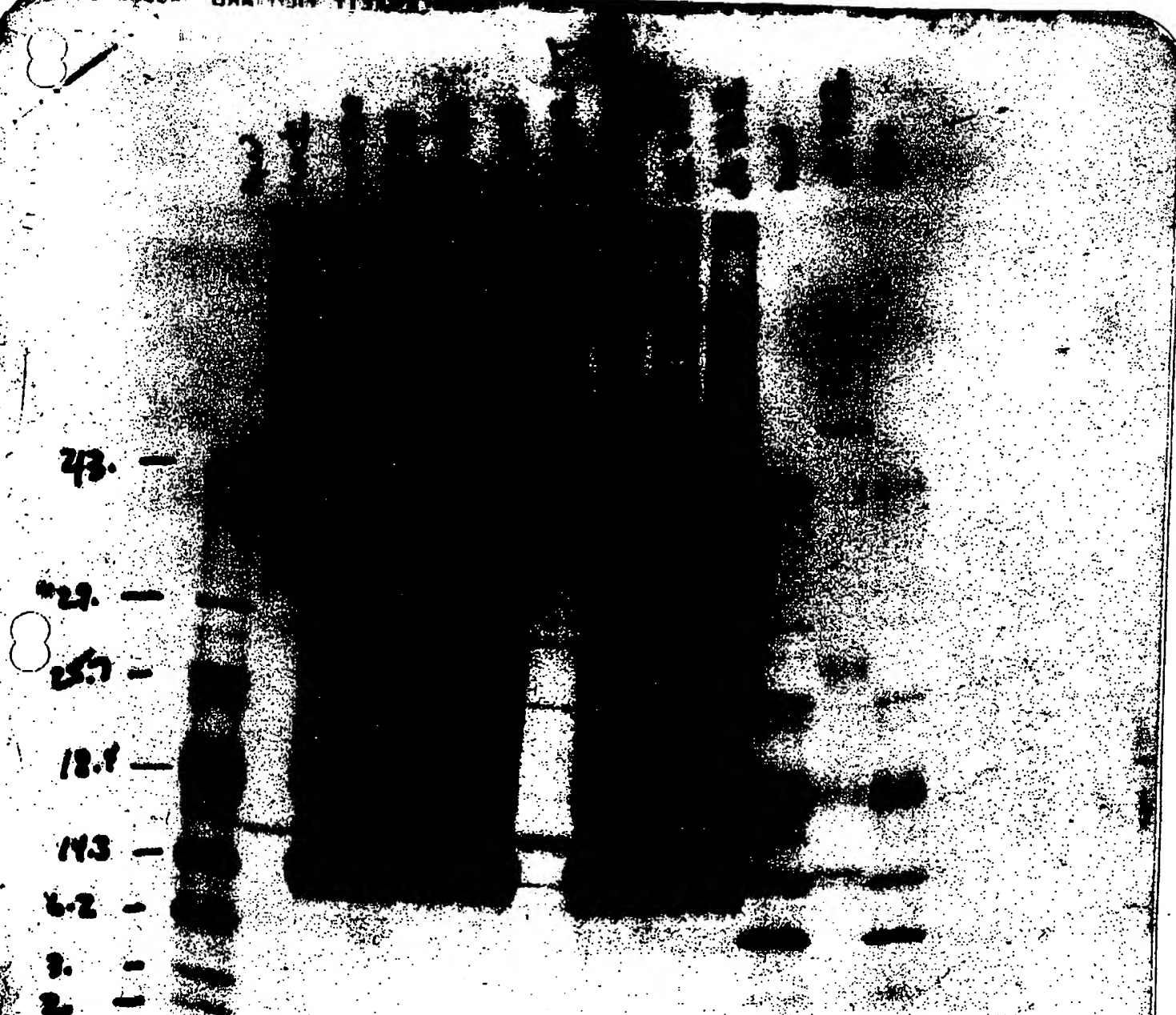


EXHIBIT
A19

Gal #1

13 day exposure
5 min developer

709 #1

11.6 (Deletion detected)

8/9 →

EXHIBIT

FROM : SAINT LOUIS UNIVER

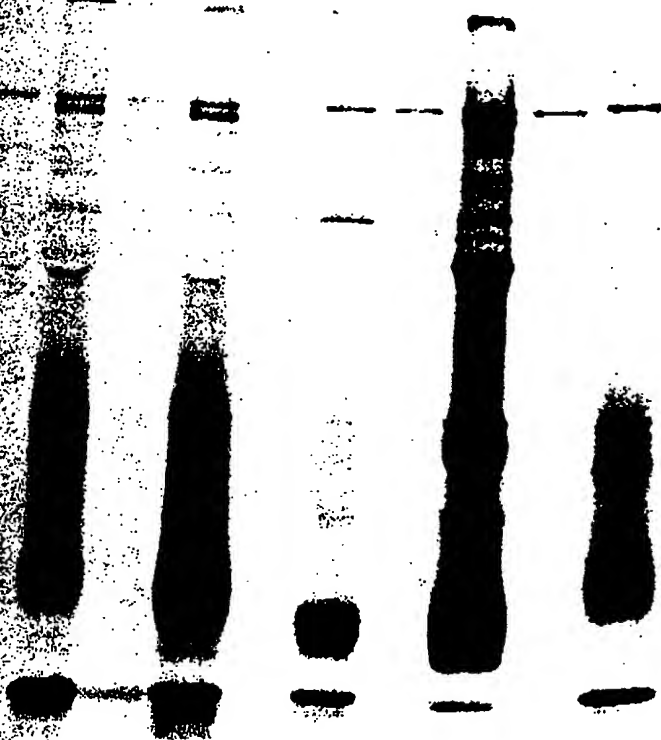
:3147733403

Dec. 19 2002 10:39AM P4

A20

7 day exposure (5 min developer)

9cc 760
db 730
db 745
db 732
db 742
db 735
db 736
db 737
db 738
Ad2



EXHIBIT

A21

Stained by A.S.

set #1

set #2

set #3

1 mock	α 11.6(2-16)	13 714	α 11.6(2-16)	25 732	α 11.6(87-101)
2 rec 700	α Fiber	14 715	α Fiber	26 742	
3 dl 712		15 713		27 735	
4 730		16 2S mer		28 737	
5 745		17 734		29 738	
6 732		18 734/MS6		30 3S-mer	
7 742		19 734/M49		31 714	
8 735		20 mock	α 11.6(87-101)	32 715	
9 736		21 rec 700		33 2S-mer	
10 737		22 dl 712		34 734	
11 738		23 730		35 734/56	
12 3S-mer		24 745		36 734/49	

1st Ab's:

α 11.6(2-16)(910830 preads 2X; 1:4 dil)
#98689 bleed out

800 μ l [(2-16)(1:200) \leftarrow 16 μ l
Fiber (1:500) \leftarrow 1.6 μ l \leftarrow mA

α 11.6(87-101)(910830 preads 4X; 1:4 dil)
#98686 bleed out

720 μ l [(87-101)(1:400) 7.2 μ l
712.8

2nd Ab's:

(all 1:50 dil's)

[α Rabbit-FITC / α Mouse-RITC]or α Rabbit-FITC

slides)

920730

Descriptions of AS 11.6K Mutants (IF)

- ① - ~~10~~ 11.6K (Z-16) (1:200 dil) (1:400 α Fiber - RITC)
- ① L - mock - ~ no background for fiber; slight background for α 11.6K (esp. for mitotic spindle poles)
R - rec 700 - all in late stage (by fiber staining); ~20-30% of cells stain for 11.6K (n.e. & Golgi primarily), some "debris" or aggregated material
- ② L - dl 712 - 100% inf'n; no 11.6K staining
R - dl 730 - 20-30% stain for 11.6K \rightarrow maybe more Golgi & debris staining; 100% infected
- ③ L - dl 745 - ~100% inf'n; poss. very diffuse Golgi staining \rightarrow not very bright & see no n.e. staining
R - dl 732 - 70-80% stain for 11.6K \rightarrow n.e., Golgi (Golgi staining reduced); a lot of aggregated material
- ④ L - dl 742 - looks ~ like dl 712
R - dl 735 - 100% inf'n; very little 11.6K staining (poss. a bit in Golgi, not really n.e.)
- ⑤ L - dl 736 - 100% inf'n; little if any staining, poss. some aggreg'd material but not definitive
R - dl 737 - 100% inf'n; bright staining; 30-40% of cells stained \rightarrow n.e., debris & virus replication sites
- ⑥ L - dl 738 - 100% inf'n; 11.6K aggregated material
R - 35-mer - " " ; not so much n.e. staining & Golgi staining is very diffuse; more e.r.?
- ⑦ L - dl 714 - ~30% of cells stained, good n.e. & Golgi but also a lot of e.r. (do not see plasma membrane)
R - dl 715 - like 714 except less n.e. staining & more aggregated material
- ⑧ L - pm 734 - like 712
R - 734/MSL - " " " " " " " "

EXHIBIT

A23

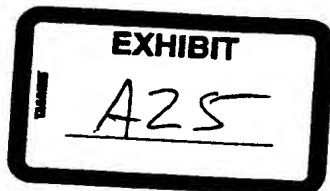
Descriptions (cont'd)

- ⑨ L-dl 713- 50-60% stained, α n.e., Golgi + a lot of e.r. - maybe more aggregated material
R- 25-mer - less n.e. staining; seemingly more Golgi staining; seemingly less staining overall
- ⑩ L-pm 734/m49 - like dl 712
#(11)-(20) α 11.6K (87-101) (1:400 dil.)
- ⑪ L-mock - slight Golgi-like pattern (very light)
R-rec 700 - ~100% stained, good n.e., Golgi; more e.r. + particulate than sometimes
- ⑫ L-dl 712 - a bit anti-nuclear (not 11.6K pattern)
R-dl 730 - ~100% of cells; very bright, maybe a bit more into all membranes (but n.e. + Golgi most)
- ⑬ L-dl 745 - more "grainy" staining + more aggregated material, otherwise quite "normal"
R-dl 732 - almost 100% with very bright n.e. staining, also Golgi + some e.r. (brighter than rec 700)
- ⑭ L-dl 742 - like 712
R-dl 735 - almost only Golgi (very reduced n.e.)
- ⑮ R-dl 737 - very bright; typical pattern but more particulate + more e.r.
- ⑯ L-dl 738 - not in membranes; some diffuse staining but mainly lots of aggregated material
R-35-mer - bright; in all membranes
- ⑰ L-dl 714 - very bright; in all membranes
R-dl 715 - less n.e. and more in plasma membrane (than dl 714)
- ⑱ R-25-mer - more Golgi, less n.e., vesicles or particles in cytoplasm
- ⑲ L-pm 734 - fairly typical but "grainier" appearance
R-734/m56 - sim to p 734 but not quite as bright
- ⑳ L-734/m49 - sim to 734, maybe more Golgi +

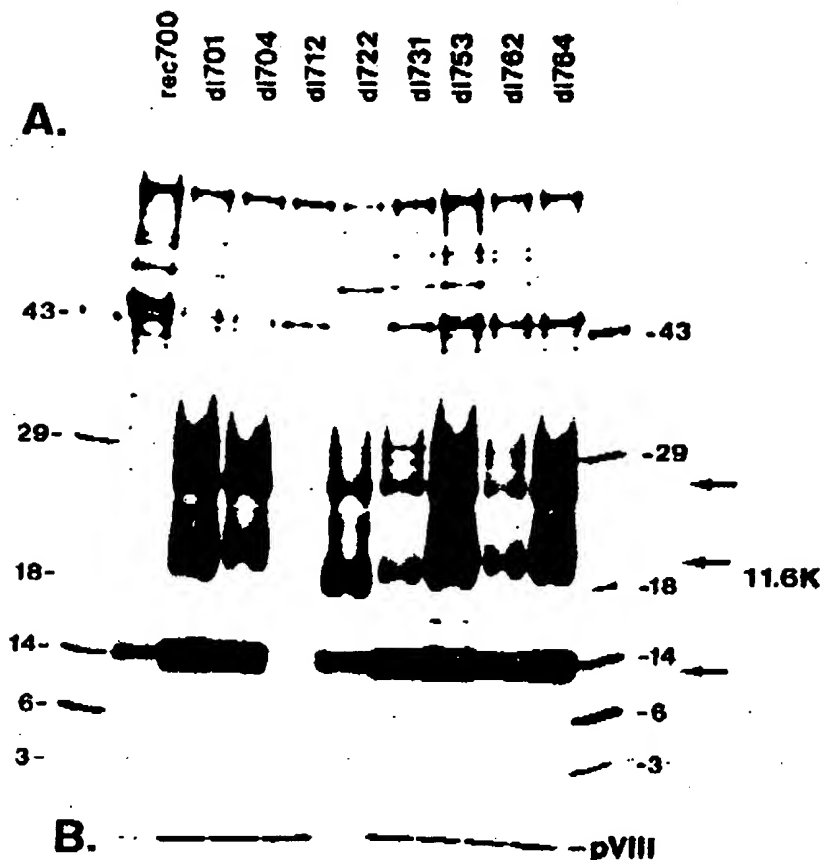
43 -
29 -
184 -
143 -
62 -

EXHIBIT
1 A24

#1 100% 4 day exposure



IF
9108271.4?
pub. 12/19/02



Have all these
prints.
Fig. 1

906331 gel #1
~ 11.6K (87-101)
like ext. v. ch

(43) #1 ← (4/12) IF to pVIII
prints

A26

(checking for 11.6.10.70)

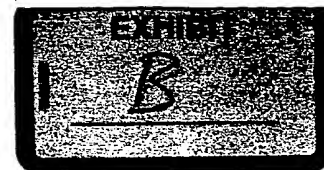
Assays of Virus Release from A549 cells

Sample #	Infection	Sample Plated cells #	pfu	Time (p.i.)	PA date	PA dilution (all 5#)
①	mock	2×10^6	—	7½h	—	—
②	mock	5×10^5	—		—	—
③	rec 700	2×10^6	10^5		(6/28) AT	$5 \times 10^0, 10^{-1}$
④	↓	5×10^5	10^5			$10^0, 10^{-1}$
⑤	↓	2×10^6	10^3			10^0
⑥	de 712	2×10^6	10^5			$10^0, 10^{-1}$
⑦	↓	5×10^5	10^5			$10^0, 10^{-1}$
⑧	↓	2×10^6	10^3			10^0
⑨	↓	5×10^5	10^3			10^0
⑩	de 753	2×10^6	10^5			$10^0, 10^{-1}$
⑪	↓	5×10^5	10^5			$10^0, 10^{-1}$
⑫	↓	2×10^6	10^3			10^0
⑬	mock	2×10^6	—	24h	(6/29) AT	10^0
⑭	mock	5×10^5	—			10^0
⑮	rec 700	2×10^6	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
⑯	↓	5×10^5	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
⑰	↓	2×10^6	10^3			$10^0, 10^{-2}, 10^{-4}$
⑱	de 712	2×10^6	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
⑲	↓	5×10^5	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
⑳	↓	2×10^6	10^3			$10^0, 10^{-2}, 10^{-4}$
㉑	↓	5×10^5	10^3			$10^0, 10^{-2}, 10^{-4}$
㉒	de 753	2×10^6	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
㉓	↓	5×10^5	10^5			$10^{-1}, 10^{-3}, 10^{-5}$
㉔	↓	2×10^6	10^3			$10^0, 10^{-2}, 10^{-4}$

at indicated times p.i., 1 ml of sup was removed, cells were pelleted (microfuge, 3 min) & sup removed to new Eppendorf; PA's of 0.5 ml volumes (single dishes); added back 1 ml of fresh DMEM (2% FCS) to each dish to replace volume removed



**SAINT LOUIS UNIVERSITY
HEALTH SCIENCES CENTER**



SCHOOL OF MEDICINE

1402 S. Grand Blvd.
St. Louis, MO 63104
314/577-8435
FAX 314/773-3403

**Department of Molecular
Microbiology & Immunology**

William S. M. Wold, Ph.D.
Professor and Chairman

Dr. Rae Lyn Burke
Chiron Corporation
Department of Virology
4560 Horton Street
Emeryville, CA 94608

Dear Rae Lyn,

I have finally returned to my office and cleared off the stack of work on my desk. Thank you for providing the names of venture capitalists, and for contacting Rajen Dalal. I have decided to take the less visionary approach mentioned in your letter of June 10, 1994, and to request funding from Chiron for the gene therapy project on the adenovirus E3-11.6K protein that promotes cell death. The proposal is enclosed. I have submitted a patent application for this project; if the patent is awarded, it would provide protection in the U.S.A. but not in Europe or Asia.

Also enclosed is a budget for the proposal. I anticipate carrying out the research in my laboratory here at St. Louis University. However, other alternatives, including doing the work at Chiron, are also possible.

I have requested a consultant fee for myself and Dr. Ann Tollefson. Ann is an Associate Research Professor working in my laboratory; she is the co-discoverer of the cell death-promoting properties of 11.6K. She will co-direct the project and she will perform benchwork on the project. Note that our consultant fees are separate from the requested budget for the project.

I am also considering establishing a corporation, perhaps in August, with St. Louis University as a minor partner. If Chiron decides to fund this project, perhaps the funding can be channeled through this corporation. Therefore, the budget for the project should be considered to be tentative.

Our Biotechnology Transfer Office requires that an appropriate official from Chiron sign a confidentiality agreement. The form is enclosed.

Dr. Rae Lyn Burke

page 2

Thank you again for your interest, and for your hospitality during my visit.

With best regards,

A handwritten signature in cursive script, appearing to read "Bill".

William S. M. Wold, Ph.D.
Professor and Chairman

WSMW:jlrm

enclosures

BUDGET

Personnel:

Lynda K. Hawkins, Ph.D.	\$20,700
TBA Postdoctoral Fellow	25,600
Fringes	9,955
Subtotal Personnel	56,255

<u>Supplies:</u>	24,000
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Other:

Maintenance contracts and repair	1,200
Telephone, postage, photocopier demurrage	400
Radiation disposal	500
Publication, illustrations	500

Subtotal other expenses	2,600
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Subtotal	82,855
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Indirect costs (10%)	8,286
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TOTAL	\$91,141
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Consultant costs*	\$12,000
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*In addition to total project budget.

CONFIDENTIALITY AGREEMENT

THIS AGREEMENT is made by and between St. Louis University Medical Center having a principle place of business located at 1402 South Grand Blvd., St. Louis, MO 63140 and Chiron Corporation a corporation having a principle place of business located.....

THE PARTIES HAVE AGREED AND DO AGREE AS FOLLOWS:

1. This AGREEMENT refers to the work of Dr.....
William S. M. Wold
relating to adenovirus 11.6K protein that functions in
promoting cell death.
2. agrees to maintain the confidentiality of Proprietary Information discussed during their meetings. Proprietary Information shall not either be used or disclosed to any other person or entity without the written consent of the St. Louis University Medical Center except as may be required under a court order.
3. The confidentiality obligation shall not apply to:
 - a: Information which can establish by reasonable proof was in its possession at the time of disclosure.
 - b: Public domain information or information which after disclosure becomes part of the public domain information by publication or otherwise except by breach of this Agreement.

The term and condition herein are acceptable to both parties of this Agreement as evidenced by the signatures of their authorized representatives:

Signature_____

Date: _____

Name: Aftab Alam

Title: Director, Biotechnology Transfer Research Center

Organization: St. Louis University Medical Center

Signature_____ Date

Name/Print_____ Title: _____

Organization:.....

ADENOVIRUS E3-11.6K PROTEIN AS A CELL DEATH-PROMOTING AGENT

A. BACKGROUND

The human adenovirus type 2 (Ad2) and Ad5 E3-11.6K protein (MW of 11,600) (Fig. 1) was first identified by our laboratory, using an antipeptide antiserum to immunoprecipitate the protein from adenovirus-infected cells (Wold et al., 1984). Subsequently, we have prepared three additional antipeptide antisera, we have isolated mutants that completely delete the gene, and we have constructed a series of about 20 mutants with truncations, small in-frame deletions, and missense mutations in the gene (Fig. 2; Tollefson et al., 1992; unpublished results). Using these reagents, we have shown that 11.6K is synthesized in low amounts during early stages of infection (prior to viral DNA replication), but in large amounts at late stages of infection (Tollefson et al., 1992). We have also shown that 11.6K is an N-linked O-linked integral membrane protein that initially localizes to the endoplasmic reticulum (ER) and Golgi apparatus, but ultimately localizes to the nuclear membrane (Scaria et al., 1992).

We have recently discovered that the 11.6K protein functions to promote cell death (A.E. Tollefson, A. Scaria, and W.S.M. Wold, manuscript in preparation). A representative experiment is shown in Fig. 3. As measured by release of lactate dehydrogenase (LDH), cells infected with wild-type adenovirus (*rec700*) begin to die at 2-3 days postinfection (p.i.), and are mostly dead by 5-7 days p.i. In contrast, cells infected with a mutant (*dl712*) that deletes only the 11.6K gene stay completely alive until 5 days postinfection, and they do not begin to die until 6 days p.i. Similar results have been obtained using, as indicators of cell death, the release of adenovirus from infected cells, trypan blue exclusion, the MTT assay (which measures mitochondrial activity), DNA degradation (agarose gels, DAPI staining, Apo-Tag), and light and electron microscopy. We believe that the function of 11.6K in adenovirus biology is to lyse

cells, thereby allowing adenovirus to be released from the infected cell.

Using our collection of virus mutants in the 11.6K gene, we are currently performing a structure-function analysis of 11.6K. Some of the mutants are shown in Fig. 2. The phenotypes of the mutants are summarized at the right side of Fig. 2. SDS-PAGE analysis indicated that all the mutant proteins are stable with the possible exception of *pm734.1* which only synthesizes residues 49-101 of the 11.6K protein (data not shown). These mutants have allowed us to map the protein domains required to target 11.6K to the nuclear membrane, and for 11.6K to promote cell death. Briefly, residues 41-59, the only hydrophobic domain in the protein, serves as the signal to insert 11.6K into membranes and to anchor 11.6K within membranes, i.e., this domain is a signal-anchor sequence. Residues 63-78, which includes the basic-proline domain (residues 63-74), a domain rich in basic amino acids and proline, is required to target 11.6K *specifically* to the nuclear membrane; mutant proteins that lack these sequences localize to *all membranes*, not specifically to the nuclear membrane. Regarding cell death, residues 1-40 and 71-101 can be deleted without abrogating the ability of 11.6K to promote cell death. Thus, the "death domain" appears to consist of residues ca. 46-60, with help from residues 61-74. However, we emphasize that although we have shown that these sequences are necessary to promote cell death, we have not shown that they are sufficient.

We do not understand the mechanism of action of 11.6K in targeting to the nuclear membrane and in promoting cell death. We believe that the nuclear membrane is the site of action of 11.6K because certain mutant proteins that do not exit from the ER or Golgi are defective in promoting cell death. Future studies in the laboratory will focus on the mechanism of action of 11.6K. This mechanism is not only of fundamental interest, but it may also

elucidate the cellular mechanisms that control cell death; this latter information may allow for novel gene therapy approaches for killing or protecting cells.

B. PROPOSAL

Since the 11.6K protein can promote the death of adenovirus-infected cells, it has the potential use as a therapeutic agent to kill cells, e.g. malignant cells, in humans. This proposed research addresses two issues that must be resolved in order for 11.6K to be used as a therapeutic agent.

First, although we know that 11.6K promotes the death of *adenovirus-infected cells*, we do not know whether 11.6K can *function autonomously* to kill cells.

Second, since 11.6K functions inside the cell, apparently at the nuclear membrane, a means must be developed to deliver the protein to the cells of interest.

C. EXPERIMENTAL PROCEDURES

C.1. Can the 11.6K protein function autonomously to kill cells?

In order to answer this question, we have attempted to isolate human A549 cells stably transfected with the 11.6K gene. Several neo^R-resistant cell lines have been obtained. These cells express only low levels of 11.6K, and the 11.6K protein is localized in the Golgi but not the nuclear membrane. Since we were not able to obtain cells that express high levels of 11.6K, or cells wherein 11.6K is localized to the nuclear membrane, these experiments suggest, but do not prove, that 11.6K can function autonomously to kill cells. We propose two approaches to address this question in more detail.

C.1.a. Tet-inducible vector.

We have obtained the *tet*-inducible vector system from Hermann Bujard

(Gossen and Bujard, 1992). In the *tet* system, the tetracycline repressor (tetR) was fused to the transactivation domain of VP16. In the absence of tetracycline, the fusion protein will bind to *tet* operators and will transactivate a promoter consisting of *tet* operators plus a TATA box. In the presence of tetracycline, the tetR-VP16 fusion protein does not bind to *tet* operators, and the promoter is silent. The major advantages of this system are that, upon removal of tetracycline, the gene is induced by up to five orders of magnitude. Also, induction is rapid, being >20% in 4 h and 100% in 12 h. Finally, the low amount (0.1 μ g/ml) of tetracycline required to keep the gene silent is unlikely to affect other properties of the cell. We will clone 11.6K into the *tet* vector, develop cell lines, and examine whether 11.6K is induced by removal of tetracycline, and whether 11.6K promotes cell death following induction. Cell death will be measured by release of LDH, trypan blue exclusion, the MTT assay, and microscopy.

If 11.6K alone does promote cell death, then we will proceed with the experiments described in Section D below. If 11.6K alone does not promote cell death, then we will proceed with the experiments in Section C.3.

C.1.b. Adenovirus vector.

There are two general classes of adenovirus vectors, nondefective and defective for replication in cultured human cells. The nondefective vectors generally have the E3 transcription unit (Fig. 4) deleted and replaced with the transgene. The E3 genes are not required for virus replication in cultured cells or in the lungs of hamsters or cotton rats, so these vectors are able to replicate. However, the E3 genes function to block the immune and inflammatory response to virus infection, so the E3-deleted vectors are more pathogenic than wild-type adenovirus.

Defective vectors generally have the E1A and E1B regions deleted and replaced with the transgene, and they have the E3 region deleted in order to increase the amount of foreign DNA that can be inserted into the viral genome (only 105% of the genome can be packaged). The E1A and E1B genes (E1B-55K) are essential for virus replication. E1A proteins are required to efficiently induce transcription of the other adenovirus transcription units. The E1B-55K protein is required for efficient transport of viral "late" mRNAs from the nucleus to the cytoplasm. Since the defective vectors lack E1A and E1B, they cannot replicate in ordinary cell lines or in animal models. The vectors can, however, replicate well in 293 cells, a human cell line that provides the E1A- and E1B-encoded proteins *in trans*.

Although E1A is required for *efficient* induction of transcription of the other adenovirus transcription units, transcription of these genes, including late genes, can occur at low levels in the absence of E1A. Indeed, recent animal model studies and Phase I human trials have indicated that defective adenovirus vectors do elicit an inflammatory response, presumably due to low level expression of adenovirus proteins.

Since we eventually hope to design an adenovirus vector to promote cell death, it will be important to limit the infection *in vivo* to the target tissue, and to minimize infection of healthy tissue. Therefore, the vector should probably be defective. The expression of the 11.6K protein could be limited to the tumor by direct injection into the tumor, or by use of a tumor-specific promoter to drive expression of the 11.6K gene. It is unclear whether the E3 genes should be included to minimize the normal inflammatory response (probably not), or excluded in order to maximize the response; this presumably would depend on the amount of infection of healthy tissue.

The design of an optimal vector is a topic of future experiments. At the present, we will use a simple "first generation" vector to address whether 11.6K expressed essentially alone can kill cells. This experiment differs from that described in Section C.1.a. because the vector will express other adenovirus proteins at low levels.

Our vector will have an Ad5 backbone, and it will be deleted in the E1A, E1B, and E3 regions. The 11.6K gene will be inserted into an expression cassette wherein transcription will be driven by the cytomegalovirus immediate early promoter, and the pre-mRNA will be processed using SV40 polyadenylation and splicing signals. The expression cassette will be inserted into the E1A/E1B region (Fig. 4), and plaques will be picked on 293 cells. Plaques of vector expressing 11.6K should be larger (more cell lysis and virus spread) than plaques from vector lacking 11.6K. Plaques will be expanded into virus stocks, and high-level expression of the 11.6K protein will be confirmed. Cultured human and mouse cells will be infected with the vector, and cell death will be monitored as described in Section C.1.a.

If 11.6K expressed from the adenovirus vector kills cells, then we will proceed with the experiments in Section D. If cells are not killed, then we will perform the experiments in Section C.3.

C.2. Mapping the minimal domain of 11.6K that is sufficient to promote cell death.

Our studies with 11.6K mutants have indicated that a protein consisting only of residues 41-101 (i.e. lacking residues 1-40) localizes quite efficiently to the nuclear membrane and is about 50% as effective as the wild-type 11.6K protein in promoting cell death. A protein lacking residues 79 to 101 is completely wild-type for localization to the nuclear membrane and promotion of cell death. These results suggest that a version of the 11.6K protein consisting

only of residues 41-78 might be sufficient to promote cell death. It is important to determine whether this is so, because such a peptide, synthesized *in vitro*, might by itself be sufficient to promote cell death (e.g. by injecting the peptide into tumors). Also, such a peptide might be less immunogenic than the entire 11.6K protein. We propose to construct an adenovirus mutant that expresses residues 41-78 and determine whether this protein can promote cell death. This mutated gene will be inserted into the *rec700* background, as we have done for all our other 11.6K mutants, and it will be expressed from the *tet*-inducible vector.

C.3. What is required in adenovirus-infected cells in order for 11.6K to promote cell death?

If the experiments described in Section C.1. indicate that 11.6K alone cannot promote cell death, then some other adenovirus gene product or some unknown aspect of the adenovirus productive infection must be required in order for 11.6K to function. The following experiments will be performed to address these issues.

First, we will determine whether 11.6K overexpressed during early stages of infection can promote cell death. The 11.6K gene will be built into our mutant, *dl7001*, which lacks the entire E3 region but expresses all other adenovirus genes. We are using this mutant as a vector to express the E3 proteins individually (Ranheim et al., 1993). Cells will be infected with the *dl7001*-11.6K vector, maintained in cytosine arabinoside in order to inhibit viral DNA synthesis and keep the cells in the early stage of infection, and cell death will be monitored.

Second, we will attempt to map the adenovirus early protein(s) that must collaborate with 11.6K in order for 11.6K to promote cell death. We will infect cells with mutants that lack the E4 region, the E1B region, and the E1A region. We already know that

this putative "collaborating" protein is not encoded by the E3 region. These experiments are similar to those we performed to map genes that function to sensitize cells to tumor necrosis factor (Duerksen-Hughes et al., 1989) and to down-regulate the epidermal growth factor receptor (Carlin et al., 1989). If we determine that an adenovirus late gene encodes the "collaborating" protein then we will attempt to map the gene using available temperature-sensitive mutants.

D. POTENTIAL FUTURE EXPERIMENTS

The following is a brief description of possible future experiments. Which experiments will be attempted will depend on the results of the experiments in Section C. Most or all of these experiments will probably require additional funding.

D.1. Design of an optimal vector to deliver the 11.6K protein to cells.

We will attempt to optimize expression of 11.6K in our adenovirus vector, and we will construct vectors with tissue-specific promoters. We will explore whether the E3 region should be included in the vector, and whether a nondefective vector might be useful.

We will also attempt to express 11.6K from a retrovirus vector. Since retrovirus vectors only infect dividing cells, such a vector that expresses 11.6K might be particularly useful to treat brain tumors.

D.2. Delivery of the 11.6K protein by direct injection.

Since 11.6K has an internal signal-anchor sequence and it has only a short sequence that is C-terminal to the signal-anchor domain, 11.6K may be able to insert into membranes in a posttranslational manner. If so, then liposomes could be an ideal mechanism to deliver the protein to the interior of cells. The 11.6K protein might integrate into the

membrane of the liposomes, become fused to membrane vesicles within cells, and then be targeted to the nuclear membrane via its specific nuclear membrane localization signal. We will attempt this experiment using 11.6K purified from adenovirus-infected cells, where 11.6K is made in large amounts. Alternatively, 11.6K could be obtained from bacterial or baculovirus vectors.

If the experiment described in Section C.2. results in the identification of a minimal domain for 11.6K to function, then the minimal peptide will be synthesized *in vitro*. The peptide will either be incorporated into liposomes or added directly to cells, and cell death will be monitored.

D.3. Coupling of the 11.6K protein to a ligand.

In one of our adenovirus mutants (*dl718*), the stop codon for 11.6K is deleted; this results in the synthesis of a fusion protein consisting of residues 1-87 in the 11.6K protein fused to residues 14-91 of the E3-10.4K protein. This fusion protein functions nearly as well as wild-type 11.6K in promoting cell death. This suggests that 11.6K could be fused at its C-terminus to some ligand, e.g. EGF, and still remain functional. If so, then the ligand could be used to target 11.6K to specific cell types that express the receptor for the ligand. Thus, the experiment would be to express the 11.6K-ligand fusion protein in bacteria or insect cells, purify the protein, add the protein to the cells, and determine whether the protein is efficiently internalized into cells that express the ligand receptor, and whether the protein promotes cell death.

D.4. Animal models.

We have found that 11.6K does not localize to the nuclear membrane in

adenovirus-infected mouse or rat cells. This may imply that 11.6K must interact with a human protein in order to promote cell death. Lack of 11.6K function in mouse or rat cells is in one respect unfortunate because an animal model will be necessary to determine whether 11.6K can, for example, cause regression of tumors *in vivo*. We will infect cells of different species, e.g. cotton rat, hamster, and monkey, and determine whether 11.6K localizes to the nuclear membrane and promotes cell death. It may also be possible to examine human tumors growing in immunoincompetent mice. When we find a species where 11.6K is able to promote cell death, then experiments will be done in this animal model.

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FIGURE LEGENDS

Fig. 1. Sequence of the Ad2 E3-11.6K protein. The protein becomes integrated into membranes via its internal signal-anchor domain at residues ca. 41-59. The protein is oriented in the membrane with the NH₂-terminus in the lumen and its COOH-terminus in the cytoplasm or nucleoplasm (the protein ultimately localizes to the nuclear membrane, but we do not know whether it is the inner or outer nuclear membrane). The site of N-glycosylation is indicated (NTT), as are the major sites of O-glycosylation. A domain rich in basic amino acids and prolines is indicated.

Fig. 2. Schematic representation of the Ad2 11.6K protein, as well as a subset of the mutants constructed in the 11.6K protein. For the wild-type protein (top figure), the major and minor O-glycosylation sites are shown, the N-glycosylation site is shown, the methionines at positions 1, 41, 49, and 56 are shown, the signal-anchor domain is shown, and the basic-proline domain is shown. Also shown is the orientation of the protein in the membrane, with the NH₂-terminal region in the lumen of membranes, and the COOH-terminal region extending into the cytoplasm and/or the nucleoplasm. The deletions shown for the various mutants are indicated by the schematic. The two right columns in the figure indicate the approximate phenotype of the mutants with respect to their ability to promote cell death, as a percentage of the wild-type protein, and their ability to localize to membranes. Membranes shown in italics are the major sites of localization. NM refers to nuclear membrane, G refers to Golgi. The protein depicted at the bottom of the figure corresponds to the putative proteolytic processing product that arises following initial synthesis of the 11.6K protein.

Fig. 3. A cell viability assay for cells infected with *rec700* (wild-type) or two mutants,

pm712 and *pm734.1*, which lack a functional 11.6K gene. A549 cells were infected with the viruses, then at different days postinfection cell lysis was measured based upon the release of lactate dehydrogenase (LDH) into the culture medium. The experiment shows that cells infected with *rec700* die (i.e. release LDH) much more rapidly than do cells infected with the two 11.6K mutants.

Fig. 4. Schematic of the Ad2 genome. The genome is a linear duplex DNA of 36,000 base pairs. *r* and *l* refer to rightward and leftward transcription, respectively. The split arrows indicate the spliced structures of the mRNAs (exons are shown). 289R, 19K, IIIa, etc. refer to proteins. E1A, E1B, E2 (A and B), E3, E4, and L1 (early) are "early" transcription units that are expressed prior to viral DNA replication. L1-L5 are families of "late" mRNAs expressed in the major late transcription unit. The 11.6K protein is translated from one of the E3 mRNAs at early stages of infection. At late stages of infection, 11.6K is translated from an mRNA that contains the major late tripartite leader (Tollefson et al., 1992).



Kostya, January 30

Project: Develop replicative vectors for cancer gene therapy.

Progress achieved:

1) 3 rounds of transfection were performed with p626 (pBHG11 with E4 promoter substituted for CMV promoter). No plaques were obtained with this construct or pBHG11 as a control. I have prepared new stock of pAV56 (left-arm plasmid) and repeated the experiment 3 times more. Now waiting for results.

2) The plasmid containing E4 promoter- SPB promoter substitution was constructed (p82). It contains DNA of dl309 from BamHI to NdeI site (E3 region from dl309) and other part to the end of genome from pBHG11 with substitution of E4 promoter. 1 cotransfection experiment was done recently with 1101/1107 cut with EcoRI and pCMV/TTF. *Not done TTF at present*

3) Cotransfection of 1101/1107 cut with EcoRI and p54 (Lynda's plasmid pdlLKH Bam-end with insertion of Ad5 ADP gene) was done. Up to now (26 days) there are no plaques with either 1101/1107/EcoRI or with 1101/1107/EcoRI+ Lynda's plasmid (parental plasmid without insert of ADP). *With p54 there are 7 plaques*. The plaques have been picked up and initial stocks of viruses prepared. Now the work is in progress to infect monolayers and characterize the genomes of this viruses. *appear in 2 weeks.*

basal 4) I failed 2 times to construct the large plasmid with mutated gp19K on dl309 background. Now repeating the cloning. *ADP inserted in XbaI site. Not start in T8.*

Proposed work:

1) To join Carol's and Mohan's work on 1101/1107 and pm975. I presume it would be interesting to do the same work on primary lung epithelial cells (GTI). SAEC - normal human lung small airway epithelial cells. *GTI get cells from GTI.*

2) Start transfection experiments on Mohan's cell line (293 transformed with pCMV/TTF) to obtain the virus with E4- SPB promoter substitution. Characterize Mohan's 293-TTF cells on their ability to transactivate SP-B promoter (transfection and IP with anti-E4 ORF6 antibodies).

3) Start the work to obtain the plasmid with E1 on 1101/1107 background? Make the point mutation as in pm975? Try to substitute E1 promoter for SPB? Enlarge the CR2 deletion?

GTI - infect cell line.

Jan 31, 97

2

Outline of Mohan's project:

1. C.F. project:

a) plasmid p Δ E1splA/3.7SPC Rep78 has ~2900 bp deletion. (Gautam's plasmid).

b) Construction of p Δ E1splA/3.7SPC Rep78 is in progress: Transferring the 3.7 SPC/Rep78 fragment to p Δ E1splA plasmid. Next week SPB/Rep78.

c) Preparation of ^{β gal assay} high titer BHK E37R Luc2 virus.
 1.4×10^9 pfu/ml. Done with 40 dishes.

Looks like virus does not grow well.
 Try again in KO cells/E1 growing in spinners.

KO/E1 - looks like may grow in spinner.

2. Cancer project:



a) Experiment 1:

a-1): Growing HEL 299 cells infected with d1101/1107.
 Showed CPE ~ 12 days.
 d1309 showed CPE on 3rd day.

a-2): Growth arrested HEL 299 cells infected with d1101/1107 did not show CPE, till 17th day. d1309 showed CPE on 8th day.

a-3): IF showed strong presence of fiber and DBP in ~ 50% of the growing cells (infected with dl1101/1107) on 14th and 17th day.

b) Experiment 2:

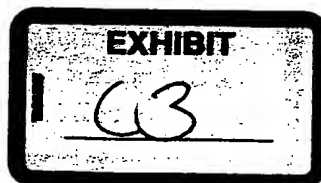
b-1): pm 975 infected growing HEL 299 cells showed CPE on 3rd day; dl 309 also showed CPE on 3rd day.

: pm 975 and dl 309 killed all the cells ~ 6th day.

: dl 1101/1107 showed CPE beginning ~ 12th day.

b-2): Till 10th day ^{17 days - still still no CPE cells frozen. Next week plaque assay.} no visible CPE was seen in pm 975 and dl 1101/1107 infected growth arrested cells.
dl 309 showed CPE on 8th day.

b-3): Growth curve = Growing and growth arrested viral infected cells are being frozen for plaque assay.



c) Experiment 3:

c-1) HEL 299 growing cells are infected with PM975; dl 1101/1107; dl 309 and mock, at MOI of 100 pfu and 500 pfu/cell. 3rd of infection, at 100 pfu PM975 showed moderate CPE and ~90% CPE in 500 pfu infection. No CPE is seen in dl 1101/1107 infected cells at 100; and 500 pfu/cell. (7th day) dl 309 showed CPE on 3rd day (100 pfu) and 90% CPE in 500 pfu infection.

Next arrested cells will be infected today.

Phage assay next week.



Gene Therapy - George M. Miller 9/10/01

Took 1 h 30 min

Karoly 2/17/97

E3 virusesDid not
make
ID, 14.7 in
EIA

- I have made cell stock of pGlc (D-) 14.7 and NPGK pp18k ap
- titring is under process (NPGK pp18k ap $\approx 10^9$)
- going to make Ad lac Pol RID and Ad lac Pol 14.7
RID in E3 region. No band in Cell.
- Bai - CMV-14.7 CMV-RID. Have done. Make virus.

FasL projectFasL
30-transfected 293
10.4/11.5 plasmid
PCR (Bai made)
also did.

- I have cloned mouse FasL in pCI, then the CMV-mFL-PolyA cassette in a left end plasmid containing p-Gal and VARNA I-II
- Transfected this construct in 293 \rightarrow the cells died
- I could not show mFL in a transient transfection assay (293 cells, Western blot with anti human FasL) but the protein could be detected in an in vitro transcription-translation reaction using the same plasmid and antibody.
- Transiently transfected MCF-7 and MCF7 Fas cells die at the same rate. No cyclo treatment is needed
- I am going to try MCF-7 Cm A first in transient transfections, then make a cell line. This cell line can be used as an "activated CTL" in Fas experiments
- I am making a Cm A-293 line

EXHIBIT

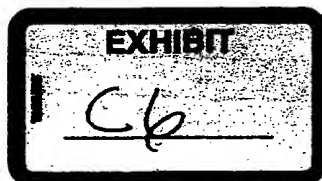
C5

Cancer Therapy project

- It seems that the W138 I use is too high passage. Only a proportion of the cells divide, the majority is senescent. I have ordered a new batch from ATCC.

February 14, 1997 Kostya

- 1) Up to now I have no plaques after transfections with p626 (E4 \rightarrow CMV promoter substitution). And I have no plaques with p84G11 as a control.
- 2) I am preparing now DNA from cells infected with 10 plaques resulting from cotransfection of 1101/1107 DNA cut $EcoRI$ with p54 (Lynda's deletion of E3, insert of ADP gene).
- 3) I have plaques after cotransfection of 1101/1107 DNA cut $EcoRI$ with p82 (E4 \rightarrow SP-B) promoter substitution. Control (1101/1107 cut with $EcoRI$) to experiment ratio is 3:10 now but in dishes with p82 plaques are still appearing (3 weeks).
- 4) I am working on Moken's cells (293 CMV/TTF), have done one cotransfection of 1101/1107 / $EcoRI$ p82 on these cells.
- 5) Cloning experiments to obtain large plasmid suitable for cotransfection with gp191C mutated are in progress.



Feb 14, 97

Outline of Mohan's Project:

1. C.F. project:

- RNA analysis of Rep78 antisense

- Hist- photograph of passage - (1st x 10⁹) filtered on 229 cells.

a) Screening colonies for 3.7SPC/Rep78 insert in pXELSP1A.

36 colonies are under screening; some colonies have the insert; screening more colonies & characterization

b) SPB promoter = PCR; strategy to clone in front of Rep78.

Mohan - KB/EAT plasmid - doing ok. still in tube (60 ml). Not in spin down yet. 293 suspension culture. Grow slow. Forms clumps at 5×10^5 cells/ml.

2. Cancer project:

Experimental #3:

(growing) HEL 299 cells: 14th day (2/14/97)

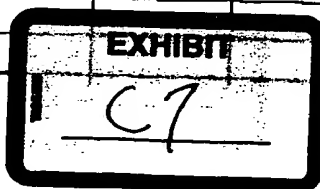
- pm 975 (100 & 500 pfu) killed all the cells.
- dl 1101/1107 (100 pfu) & CPE starts in 500 pfu - shows CPE. (better than 100 pfu)
- dl 309 (100 & 500 pfu) killed all the cells.

Growth arrested HEL 299 cells: 7th day

- No CPE in dl 1101/1107 (100 & 500 pfu);
- No CPE in pm 975 (100 pfu); CPE shows in 500 pfu. Same as 309 at 500 pfu.
- No CPE in dl 309 (100 pfu) CPE shows in 500 pfu.

Growth Curve:

Dishes are processed; going to do plaque assay



Kathy 2/14/97

E3 viruses

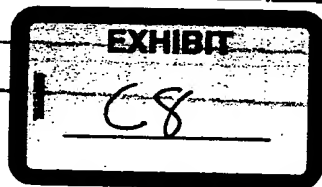
- Titer of V P6K pp19k_{exp} is 1.37×10^9
- β Gluc(D-) 12.7 is less than 10^7 (?) (see repeat titer exp.)
- We are trying to make virus with the plasmids made by Bai
- We are assaying for expression of 12.7 and R10 in a Western

FosL project

- I tried the infection-transfection experiment twice. I failed both attempts because the virus killed the cells before I could transfect. I used 50 pfu/cell (233), 20 μ g/ml Ara C. The cells were rounded up after 18h (1st exp.) and 7h (2nd exp.) 5 PFU. MCF7 cells. Fetal supernatant. 293/cmA cell line.

Cancer Therapy project

I have got W138 from ATCC. I am growing them up. Got cell proliferation bet-strain for BudR.



Kostya

1) I have made and analyzed by restriction and
 per ~~PCR~~ Hirt DNA preps from S' of 10 plaques
 that I had after p54 ^(Lynda's plasmid + ADP) cotransfection with 101/109/R1.
 2 plaques were wt with addition of something
 that I suggest is defective version of recombinant
 virus. 3 other plaques contain E3 from p54.

2) I'm ^{Have 10 plaques - half small, half very small. One in with. The transfection was complicated.} picking up plaques resulting from ^{CO-transfected Ceder-} transfection
 of p82 (E1k → SP-B promoter substitution). ^{cut 8/10/11/07}
 Exp't is being repeated - exp't is 3 weeks old; Had same plaque. ^{also Transfected TFF1.}

3) Failed to construct large form of gp19K *
 plasmid due to contamination of competent cells
 with something AmpR. Now prepared new batch
 of competent cells, about to repeat cloning.

AD/ADP recombinant in "Lynda's plasmid, a E3, + C1, deletion extending like p30011.
 Has 4 plaques, 2 are recombinant (Hirt, per), 2 seem to be mix of wt and recombinant
 with a deletion. These plaques give strange appearance, as if they are secreting
 a factor that kills surrounding cells - true
 Lynda's plasmid - not even sure that G4 is present.

Kostya - will plaque-purify the "mutant" and "mixed" plaques.

↳ The two mutant plaques are very slow - may not be good tailer virus.



New Energy Group Meeting 920221

(PCI) CMV-^{wt} gene - SV40 poly A
Koroly 2/21/8

ES viruses

- Western with the pCI R1D and pCI 14.7 plasmids
was negative - I am doing an IP in pAETSP1A
- These are the constructs that Dai made.

FasL project

- The shedded mFasL is not toxic
- I am trying to make virus with mFasL in left-end plasmid and dl7001

It is known that the human FasL is ^{shedded} toxic, the ~~mouse~~ FasL is not. Killing by FasL is very fast.

All MCF-7 cell lines die when transfected with vector/FasL except the one in Crnt.
They die in one day.
25-50% of the cells die.

Will do exp in MCF-7/14M cell line.

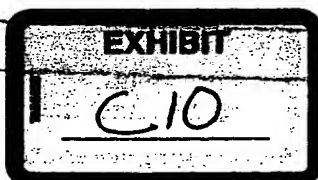
Try any MCF-7 cell line expressing R1D2 or R1D3?

Could try to repeat this exp in A549, even if transient transfection is poor.

Karl-making 783 cells expressing Crnt.

MCF-7/Crnt/FasL - have colonies.

- Transfect with R1D + LDNGFR, purify, then transfect with FasL.



Mohau's project.

Feb 21, 97

1. CF. Project:

- a) Final plasmid p Δ ELSP1A/3.7SPC Rep78 has been constructed; plasmid preparation is under progress.

2. Cancer project:

Experiment #3:

Growing HEL 299 cells 21st day

- a) d1101/1107 shows better CPE in 500 pfa than 100 pfa.
- b) pm 975 & d1309 killed the cells.

Growth arrested : 14th day

- a) NO CPE in pm 975 (100 pfa).
At 500 pfa at 14th day cells are killed.
BPE starts at 3rd day in confluent area. Cells dead at 12 days.
- b) NO CPE in d1101/1107 (100 & 500 pfa)

Growth Curve:-

pm 975 - infected G & GA. HEL 299 cells.
Growth Curve is done; waiting for plaques.
Will need to do growth curve for d1101 - will do next week.

Northern blot will be done for Rep78 antisense cell line
Trying to clone SPB/Rep78 into p.



23-28-97 Kostya

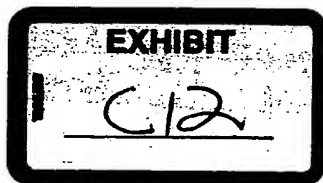
Need to do Hirt on some of these plaques.
1) I have analyzed by PCR 8 of 10 plaques which I had after 1101/1107 cut with EcoRI + p82 (E4 → SP-B promoter substitution, E3 from dl 309). They all contain wt E4 prom. And I have no up to now plaques with p626 (E4 → CMV promoter substitution, E3 from pBK611). Determine RHE sequence of Nishida's plasmid.

1) I am going to put different variants of E3 that I have in ~~other~~ ^{small} plasmids (dlE3 X60 + ADP, dl 309 with gp19K unmutated, wt?) into Linda's plasmid with which I have obtained a recombinant virus.

1) I would propose to start the work toward E1 promoter deletion and substitution with SP-B or any other tissue-specific or tightly regulated promoters. As alternative we can try to substitute E2A promoter.

1) Growing up ADP mutants vector.

BLAST lipoxygenase - 3 diff species.

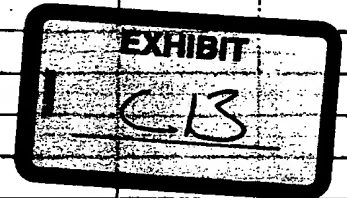


Mohan,

Feb 28, 97,

1 C.R. Project:

- a) Preparation of pSEISpIA/SPC Rep78 is progressing. Some problem in CsCl banding. Repairing another prep. Saw 4 bands - good band.
- b) Construction of SPB-Rep78 plasmid.
: partial digestion of p3.7SPC/3540 with HindIII -



2. Cancer Project:

Experiment # 3:

Growing HEL 299 cells 28th day

1101/1107
good CPE
at 500 pfu

- a) dil 1101/1107 shows CPE in 500 pfu and 100 pfu

Growth arrested cells: 21st day.

- a) pm 975 at 100 pfu shows ~ CPE?
- b) NO CPE in dil 1101/1107 (100 & 500 pfu)

Growth Curve: pm 975 100 pfu. On 293 cells.

Growing:

3 rd day	= 7.1×10^4 pfu/ml
5 th day	= 1.3×10^5
6 th day	= 1.1×10^5
7 th day	= 7×10^6

Growth arrested:

1101/1107
assay has been
standardized.
Need to stain next week.

Need to check 1st & 3rd day.

10 th day	= 1.2×10^5 pfu/ml
14 th day	= 3.2×10^5
19 th day	= 1.8×10^5

K13/E1A are
Growth arrested
Growth arrested
Not proved that it.
293 cells
Froze Microbot.
from

Keroly 2/28/9

E3 viruses

- 3 transfection going. No plaque yet. 11/01/18 day 10. BH611 BH610. Try 10. BH610-plaque on 16.12.02
- IP with Bai's constructs: I could IP 14.5 (and 10.4?) from an in vitro translated sample. After one day exposure the transfected samples did not show up. The 14.7 plasmids were negative even in the in vitro translated samples. Sequencing is under process. 10.14.7th made cell stocks of Krigen's two plasmids p-Gal-PGK14.7th and p-GalR10th. I am going to try to make virus with them.

FasL project

- Have McF7-FasL clones. I have transfected R10 and mFasL (both in pCI vector) in 293 cells. Result is due this evening tomorrow morning.
- I have infected 293 cells with the CPE stock from the d17001 infection - LEMFL transfection experiment.

Cancer therapy project

- I use the new K138 cells for a new round of infection with 1101/1107.

I need to call Bruce Trapnell. What is real status of money.



3/7/97 Kostya

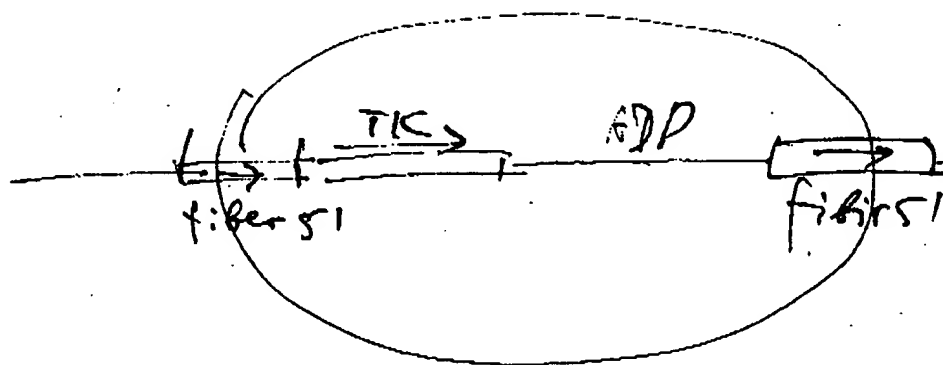
- 1) Cloning of ITR PCR product to p82 (EU-SPB promoter plasmid) is in progress.
- 2) I have a problem with TK, cannot PCR it from Linda Morrison's plasmid. If it is possible, I would like to have a plasmid with HSV-1 TK gene from GT1.

- 3) Plaque assay of S24 (vims with Linda's E3 deletion + ADP insert) on 293 cells.

(309, 1104/1107) (wt control) ^{Linda's deletion}
 12.5K, 44 polyA
 into mutate retains

(S24) develops plaques a bit slower than wt, plaques appeared 1-2 days later than in wt, day 16 - plaques are ~ 8-10 mm in diameter.

(7001) - plaques are tiny (1-2 mm) at day 16.



03-07-91

Kostya

i) Results of cotransfection 1101/1107 /EcoRI + p54 (dlE3 + ADP) → 4 more plaques were analyzed. 3 of them contain recombinant genomes.

ii) Subcloning of dl 309 E3 with gp19K mutated and dlE3 Xba + ADP into Lindel's plasmid is in progress. When the plasmid with 19K* is made I'm going to insert HSV-1 TK into PacI site created in gp19K gene.

i) No plaques with p82B (p84611 E4 promoter → CMV promoter).
No plaques with p84611 as a control.

ii) 4 more plaques resulting 1101/1107 /EcoRI + p82 (E4 → SP-B promoter) were analyzed. All contain wt genomes.

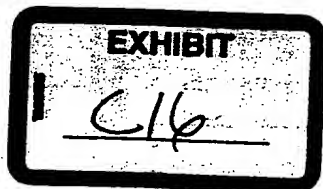
iii) In 2 repetitions of cotransfection 1101/1107 with p82 (E4 → SP-B promoter) no plaques neither in control nor in experiment. 2nd experiment was done on Moken's

293/CMV-TTF cells.

Now repeating the cotransfection.

iv) Sequencing of Nippen's plasmid p21 (E4 promoter dl) is in progress to prove that right Ad ITR is intact in the plasmid.

v) Growing initial stocks of the recombinant virus with dlE3 + ADP.



Kathy 3/7/97

E3 viruses

- I have transfected p-Gal PGK 147 ep and p-Gal PGK R1D₉ (with BH611) I am waiting for plaques.
- Still no plaques - Bai's constructs. Now 3 weeks old.

Fasl project

- The pC1R1D construct did not protect against killing induced by pC1mFasl transfection (293 cells)

Exp 1 - Transfect with 5 μ g R1D

- wait 24 h

- Transfect with 5 μ g mFaslExp 2 - Transfect with 5 μ g R1D

- wait 24 h

- split the cells

- wait 24 h

- transfect with 0.5, 1, 2, 5 μ g mFasl

- The MCF7 147 cell line (Terry) is not protected from killing with mFasl.

- I am trying to show functional R1D in transfected cells (IP, IF).

- I am ~~also~~ trying to show 147 in Terry's line (IF).

- I am expanding colonies isolated from 293Gm A and MCF7 control mFasl transfections

- I am growing up virus (putative mFasl - p-Gal 7001) isolated from blue plaques.

Cancer therapy project

- 11/01/07 on U138 growing 10th day, arrested 7th day - no difference (no CPE). It seems that there might be a diff.

EXHIBIT

C17

Mohan, March 7, 97

1. C.F. Project:

APU-JIR - KB/EI growing
CHY800000.

- Preparation of plasmids p Δ E1sp1A/SPCRep78 and pBR640: under dialysis.
- Construction of SPC-Rep78 plasmid - partial digestion to preparative scale.
- RNA blot: for antisense Rep78 RNA in progress.

2. Cancer Project:

Experiment #3:

- Growing HEK 299 cells 35th day
- DI 1101/1107 shows CPE in 100 & 500 pfu.

Growth arrested: 28th day

- pm 175 at 100 pfu shows CPE.
- No CPE in DI 1101/1107 (100 & 500 pfu)

Growth Curve: DI 1101/1107 (100 pfu) Total cell + supernat

Growing:

5 th day =	1.4×10^4	pfu/ml
15 th day =	4×10^4	"
24 th day =	1.3×10^6	"

Growth arrested:

5 th day =	1.1×10^3	pfu/ml
10 th day =	1.4×10^3	"
19 th day =	8.4×10^3	"
23 rd day =	5.6×10^3	"

Do 309

pm 175 growth arrested
day 1 + 3
will be titrated
next week.

Growth Curve: pm 175 growth arrested day (1 + 3) are titrated.

EXHIBIT

C18

I E3 region:

i) Initial stocks of the viruses with dlE3, ADP insert are prepared. Plaque assay on 293, A549 cells with 1101/1107, dl309, ADP⁻ viruses as controls is to be started.

ii) Two large plasmids suitable for cotransfection with viral DNA based on Lyde's plasmid with E3 a) from dl309 with sp19K unmutated b) dlE3 Xba + ADP^{K03} are made.

CsCl preps of these plasmids are done. Cotransfection of these plasmids with 1101/1107 DNA / EcoRI is in progress. Will do one in TK gene, and PacI site.

II E4 - SP-B promoter:

i) There were 4 plaques which are developing CPE very slow in plate wells (Incomplete CPE in 3 weeks).

ii) Alternative project: E1 → SP-B (SP-C) promoter substitution. There was an article by David Solnick with E1 → MLP substitution (deletion E1 promoter -45 → +8 relative to E1 cap site).

However, I would propose to try to express E1A under the control of SP-B or SP-C in place of standard E1 deletion. Advantages: a) E1B would be completely deleted in the virus b) It is possible to use 13S cDNA (express only 289 aa E1A)



Kordy 3/14/

Fasl project

- I did an IF with A548 and 293 cells transfected with pCOV43 RID α , pCOVARIDP (alone and together) and pCIRID. The results are inconclusive. I could see ^{strong} RID β expression where it was present, but the localization was mostly Golgi, even if RID was supposed to be there. (This was not easy to judge in 293. The IF did not work in A548). The EGFR internalisation did not work because of the antibody. I am going to repeat this experiment in MCF-7.

- I have labeled IP RID β , but for co-IP of RID α . I have not processed them yet.

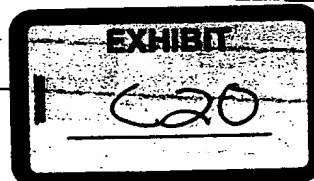
- Fasl virus: I am doing a plaque assay with the isolated, blue⁺ viruses.

Starting to test 293/empty clone. Enough antibody? Transfect: Fasl-see if survival.

Cancer Therapy project

- I am doing an IF ^{→ DAPI, Biotin incorporation} with 1101/07 infected U138.
- Growing U138 infected with 500 pfu/cell 1101/07 shows no real cpe on day 15.
- Growing U138 infected with 100 pfu/cell, 1175 shows cpe on day 3.

1101/1107 does not grow on primary cells. Perfect.



Gene Therapy Group Meeting 970314

Mohan, 3/14/97

1. C.F. Project:

- a) pDEISPIA/3.7 SPC Rep78 has one additional Koz1 site;
Co-Transfected with pBM610 in 293 cells.
- b) Give to Follen-Waters for GIB and GIB-19K.
- b) KB MMT E1 Spinner cells, frozen same. ^{MTV promoter. Replicate} _{cell banking =}
- c) RNA (293 Rep78) - transferred; synthesizing the RNA probe in progress.

2. Cancer project:

Growth Curve: pm 975 Growing:

total Cells Day 1 = 8×10^4 pla/ml (New) Day 1 & 5
 plasma supernatant 3 = 7.1×10^7 309 is now being titrated.
 " 5 = 1.3×10^7 Day 6 - all
 " 6 = 1.1×10^7 all on floating.
 " 7 = 7×10^6 "

Growing:

Day 1, d1 1101/1107

Day 3, d1 1101/1107

Day 1, d1 309

Day 5, d1 309

These points
are being
titrated by
Stain Next week!

Growth arrested:

GA 1 DAY = d1 1101/1107

GA 1 Day = d1 309

GA 5 Day = d1 309

Need to call Bruce.

EXHIBIT

C21

3-21-97

Kostya

1) Sequencing of p21 (Nrippen's plasmid, EcoRI-B fragment of pBUG11, EU ^{12-14 kb} promoter deleted).

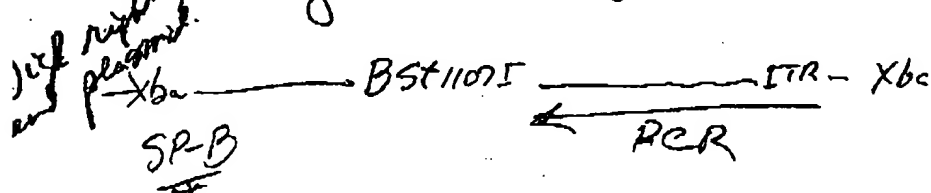
Primers directed to deletion point. ^{SalI} ^{SP-C} ^{SP-B} ^{CMV}

i) Ad5 sequence is OK ~ 600 bp downstream the deletion.

ii) Upstream the deletion Ad5 sequence 35770 → 35858 is as predicted. Upstream of Ad5 35858 there is sequence which is ^{transposon 5.} ^{in ITR.} *E. coli* Tus according to BLAST.

Probably, ITR is in plasmid but it can not be concluded from this sequence. Moreover, even if it is there, Tus is inserted - 77 bp from the right end of ITR ^{Tus is at least 500 bp or more larger.} making it not recognizable to virus.

2) It is possible to cut out defective sequence from p82 (large plasmid with SP-B promoter) with Bst 1107 I and Xba I and put PCR product corresponding to Ad5 right ITR in single cloning.



Nrippen-site in
Gal4 promoter.
Review Gal4 project.



Karoly 3/23

FasL project

- I have transduced 12 283 crmA clones and got partial protection in 7 of them. I will run a Western blot.
- I have tested 15 MCF7 crmA-mFL clones in a Western blot (using a hFasL). All seem to be negative. I will try mixing experiments.
- mFasL viruses: no blue plaque in 2nd plaque purification.

Cancer Therapy project

- Growing V138 infected with 500 pfu/cell 11/01/02: no CPE and
- Arrested V138 infected with 100 pfu/cell on 9/5: no CPE and
- Cell proliferation assay (BrdU incorporation \rightarrow IF) shows that growing V138 is not really growing.

EXHIBIT

C23

Mohan, 3/21/97

1 C.F. Project:

1st transfection was done last week
 a) 2nd transfection was done in 293 cells;
 pBHG-10 + pAE1Sp1A/3.7 Sp1 Rep78

b) Northern Blot: for 293 Rep78 cell line, expressing
 Rep78 antisense RNA; blot is exposed to film.

c) checking E1 expression in KB MUTV E1 spinner cells. Cells were
 induced by dexamethasone → samples given to Tander
 Grow E1/EB cells. Start 5 BTR

2 Cancer Project:

Growing 1 day: $d(1309) = 4 \times 10^4$ pfu/ml
 5th day: $d(1309) = 4 \times 10^6$ pfu/ml

Growth arrested: 1 day $d(1309) = 1.4 \times 10^5$ pfu/ml
 5th day $d(1309) = 1 \times 10^6$ pfu/ml

Growing day 1 = $d(1101/07) = 4 \times 10^4$ pfu/ml

Growth arrested day 1 = $d(1101/07) = 1.2 \times 10^3$ pfu/ml

Buy spinners from MG

EXHIBIT

C24

Growth Curve HEI 299 cells

Growing:		pm 975	d1112/	d1319	pfu/ml	all (100 pfu)
Day 1		8×10^4	4×10^4	4×10^4		
" 3		7.1×10^7				Repeat @ 500 PFU
" 5		1.3×10^7	1.4×10^4	4×10^6		Do ~ 3-10 h - to identify early round
" 6		1.1×10^7				More CPE data @ 500 PFU
" 7		7×10^6				
10						Read - next week @ WI 38
15			4×10^4			
19						
23			1.3×10^6			
24						
Growth arrested	days					
	1		1.2×10^3	1.4×10^5		
	3					
	5		1.4×10^3	1×10^6		
	6					
	7					
	10	1.2×10^5	1.4×10^3			
	14	3.2×10^5				
	15					
	19	1.8×10^5	8.4×10^3			
	23		5.6×10^3			

EXHIBIT

C25

Mohan, 1/4/97

1. C.F. Project:

a) 3rd Transfection was done; ~~3 transfections are automatically~~ pBHG10 + pΔE1spA/3.7SPK Rep78
 Next week 18-20 days, should start seeing plaques.
 (Chem 1st transfection) On 293

b) Northern blot: 293 cells expressing antisense Rep78; RNA from 293 cells itself, gave hybridization signals (bands) with sense and antisense Rep78 RNA probe. May be RNA contamination? or unspecific bands?

293 cells transfected again \bar{c} Rep78 antisense (pCDNA3 Rep78); when the G418 resistant colonies form, individual colonies will be propagated for the above RNA studies (or PCR).

c) checking expression of EI in KB MMTV EI spinner cells.

i) KB MMTV EI cells induced with dexamethasone expressed EI B 19K; for EIa expression the antibody (-Tudor) is not good.

ii) I made a B46 E3 ITR LacZ virus prep from KB MMTV EI spinner cells (~1.5 liter); so EI is functional in this KB MMTV EI spinner cells.

iii) From 3 liter KB MMTV EI spinner spf, 8.15 AM dexamethasone for 3 hrs gave viral band same as above

2. Cancer Project:

Experiment 3: HEL 299 growing and growth arrested cells are infected with Δ116/mt; Δ1309 (500 pfa/cell) = under progress for Growth Curve experiment.

Need graph/table for trip to G.I.

EXHIBIT

C26

FasL project

- I did a Western with the 293 c-met clones, they all express c-met. I will cotransfect them to make FasL virus.
- Use this cell line to make Ad-FasL vector, perhaps Ad-14.7k and Ad-RID vectors.
- Transfect FasL into cells. 1st exp - got protein.

E3 proteins

- I have isolated plaques from CMV RID and CMV 14.7 transfections and VRID and V 14.7 transfections.
Neigen RID
Pot promoter, R → L orientation
- Expression of RID from the CMV RID construct is ~~not~~ not proven yet.

Cancer Therapy

- I am liking 1101/1107 yields on V138
- There is some CPE in gm875 (100 pfu) infected V138 on day 15

Make Ad vector (gene therapy) that expresses c-met.
Use for gene therapy to keep transduced cells alive.

Lynen's expression cassette

all promoter, all Ad E3 genes. 1st 293, then MXF-7.
Do IP

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



EXHIBIT

C27

4/11/97 Kostya

- 1) Cotransfection of 1101/1107 / E10R1 + p101
(dl309E3, gp19K mutated) or p111 (dLE3X6a + ADP):
There are 1 plaque with 101 and 1 plaque with 111
and no plaques in control dishes. Now amplifying
these plaques to analyze the genomes.
- 2) Need TK HSV-1 gene from GT1 (if possible, with
sequence and plasmid map). I'm going to insert
the TK gene in PaeI site of p101 (in gp19K gene)
and XbaI site of p111 (~~between~~ upstream from
ADP insert).
- 3) Failed once to replace TnS sequences with
ITR in p82 (dLE4 promoter, SP-B promoter insert),
now repeating the cloning.

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



Mohan 4/11/97

Gene therapy Meeting1. C.F. Project:

- a) Three different transfections were done to ~~make~~ ^{construct} ~~constra~~ ^{construct} Rep78 virus. No plaques - yet in ~~one~~ ^{transfection} transfection (24 days)
- b) dishes showed CPE like? in ~ 16 days; plaque titrations were done. started 4-11-97
- c) 293 ~~Rep78~~, antisease cell line were brought from the freezer; going to repeat the above transfections in Rep78 As₂ cell line.
- d) primers are ordered for checking ~~ATV~~ ^{ATV} Rep78 in 293 cell line.

2. Cancer project: HEL 299 cells, 500 pfu.

- Growing cells showed good CPE at ~ 15 days (4/11/02)
- Growth arrested cells ~ 11th days very little CPE!
- dishes are being frozen for growth curve data

3. KB MMTVEI:

pBabe puro plasmid is under preparation for Co-transfection with ~~EL~~ ^{EL} plasmid; pCma plasmids

EXHIBIT

C29

Hoechst-sprink, Cell stock, titer 1.4×10^7

Keroly 4/11/87

Do I? of this vector, compare to A15.

E3 proteinsNeed
to repeat

- Tested two MPK 14.7 viruses for β -gal - one expresses.
- Tested 3 CMV 14.7 and 4 CMV R10 viruses for β -gal - none of them expresses.
- I have tried to sequence the CMV-R10 construct, did not work. Lyndy - point mutation in entire E3 region of A15. Need to do this, on a promoter.

FestL project

- I have a ^{mixing} ~~sandwich~~ experiment running with MCF7 - LinnA - FestL cells, so far it is a may be.

Cancer Therapy

Preliminary titers:

Growing ^{U138} ~~U138~~ infected with 500 pfu/cell 1101/1107

D4	<	10^5
D3	\approx	1×10^5
D7	\approx	3×10^5
D10	\approx	2×10^5
D15	<	10^5
D20	\approx	8×10^5
D25	\approx	1.5×10^6
D30	\approx	5×10^5

Quiescent U138 infected with 500 pfu/cell 1101/1107

D15	<	10^5
D20	<	10^5
D30	<	10^5

no plaques at 10^{-5} dilution.

Will have A15 data on U138 next week.

EXHIBIT

C30



4/18/97 Kostya

- 1) Plagues, resulting from p101 (gp 19K mutated) and p111 (XbaI(E3 + ADP): I have Hirt preps of genomes of these viruses, now analyzing by PCR and restriction digestion.
- 2) I have got clones with T_uS → ITR substitution. Going to analyze them.
- 3) Starting to construct plasmids with Ad5, 760 RID genes under the control of CMV promoter. Same with the 14.7 gene.

Kostya will put E3 transcription unit, containing the pm 794.1 ADP mutations, behind the CMV promoter, for the purpose of inserting into E1 region of BAC11 (or 10).



1X.enrln 4/10/34

E3 proteins

- I am going to test more MP6K 14.7 and MP6K R10 viruses. (I am infecting today)
- I did an IP with MP6K p18K virus, no band on ON exposure.
- I have got the oligos for sequencing the CMV R10 construct, I will do it this weekend.

Fast project

- I am growing up 293 cells and making a (S1) stock of the phage (CMV in Fas L in left hand phage)

Cancer therapy project

Preliminary letters WI-38

	1101/1107 500 PFU/cell		975 100 PFU/cell		308 100 PFU/cell	
	A	G	A	G	A	G
D1		1×10^5	1×10^5		3×10^6	
D3		5×10^5				
D5			1.5×10^5		1×10^7	
D7		3×10^5				3×10^7
D10		4×10^5	1×10^6			
D15	$< 10^5$	$< 10^5$	2×10^5			
D20	$< 10^5$	8×10^5	8×10^5			
D25		2.5×10^6	7×10^5			
D30	$< 10^5$	7×10^5				

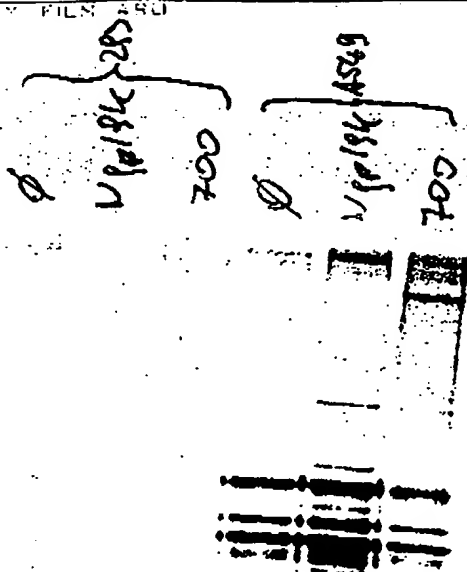
EXHIBIT

C32

KODAK SAFETY FILM 340

KODAK SAFETY FILM 340

4/18



Could see by IF, beginning at 2 dup pi

EXHIBIT

C33

Moham, 4/18/97

1. C.F. Project:

- a) No plaques in 293 cells co-transfected with pBHG10 and pAE1Sp1A/3.7 SPC Rep78. (~ 30 days and 24 days); 3rd transfections (~ 18th days) dishes are stained; waiting for plaque plaques.
- b) Cells showed CPE like effect (pBHG10 + pAE1/SPC Rep78) were titrated and not stained yet. But even undiluted dish did not show CPE.
- c) RT-PCR showed no Rep78 DNA fragment in 293 and 293 (Rep78) AS cell lines.
- d) Spinner KB MTV E1 cells - Virus IR LacZ is under in spinner; Karl virus is going next.
- e) pBabe puro plasmid is made in large quantities; for transfecting the KB E1 cell lines with Et and CreA plasmid separately.

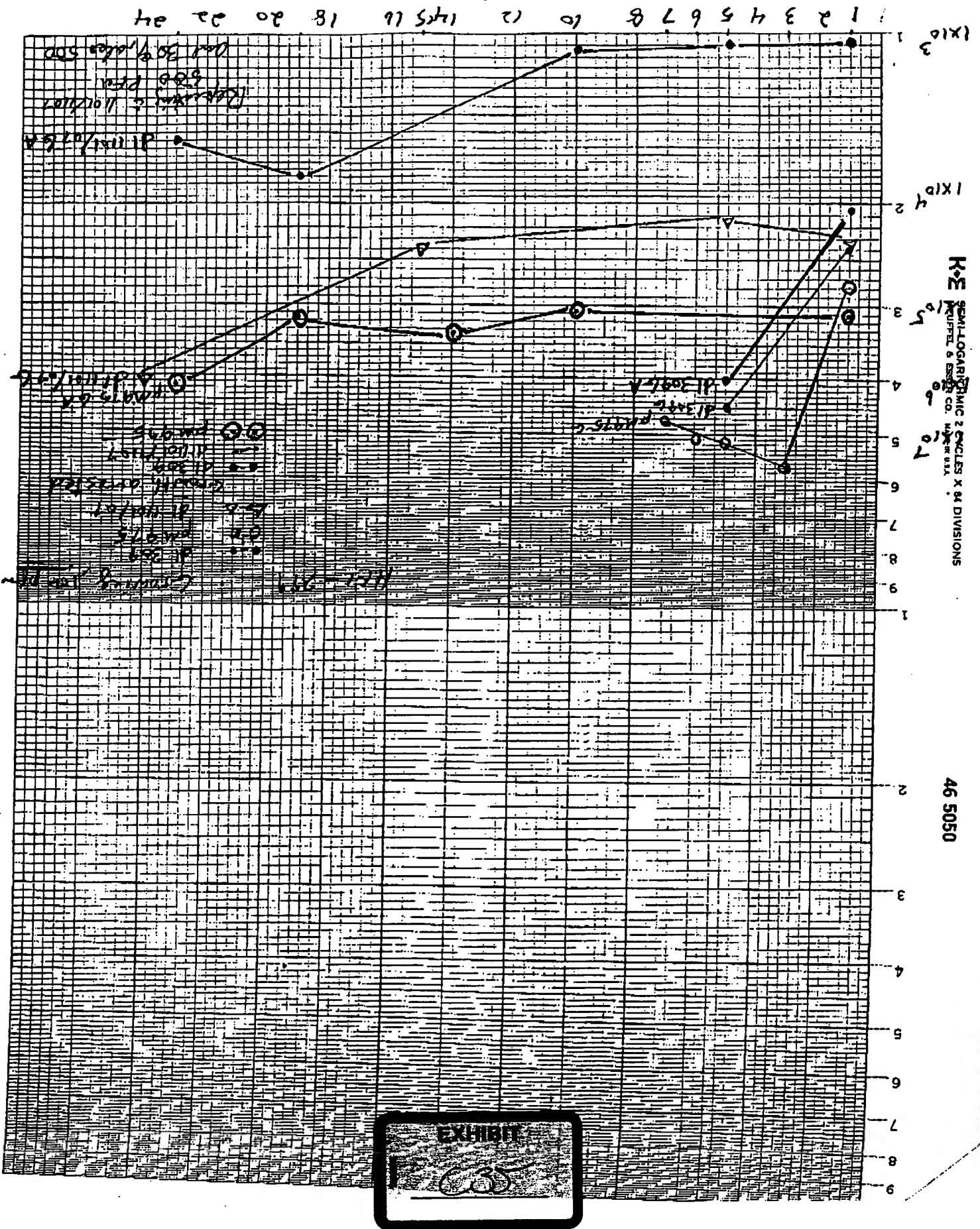
2. Cancer project:- HEL 299 cells; 500 pfu
- Growing cells were dead at ~ 21 days.

- Growth arrested cells 18th day. On 21st day cells will be frozen for Growth Curve analysis.

3. preparations: plasmid BHG10, BHGE3, pAE1/SPC Rep78; will be for transfection. Cells purified.
293 (Rep78) AS cell line will be co-transfected &
BHG10 + pAE1Sp1A/3.7 SPC Rep78 plasmids
BHGE3
KRE DNA

EXHIBIT

C.34



4/25/97 Kostya

- 1) I have got the virus 1101/1107 with gp19k mutated (restriction digestions and PCR).
- 2) Now preparing Hirt's from 4 plaques which should be 1101/1107 E1; Xba E3 deletion, ADP insert.
- 3) Failed to substitute Tsr → ITR. Going to do it in 2 clonings but without partial digestions.
- 4) Sequencing shown that ITR is OK in Lyda's plasmid; could not sequence through ITR-ITR junction in pUC10, 11; I have repeated the sequencing with different PCR protocol, now waiting for results.
- 5) I have checked with Ann, she doesn't have plasmids with rec 700 or pm 734.1 which would be suitable to cut out SrfI - NdeI fragment corresponding to whole E3, but she does have the viruses. Now going to prepare rec 700 and pm 734.1 DNA to insert SrfI - NdeI fragment to pCDNA3 / EcoRV site.
- 6) The virus 544 (1101/1107 E1, Lyda's deletion of E3 ~~(1101/1107 E1)~~, 12.5 k ATG mutated, d127984-28153 d128390-30883) + ADP insert into PaeI site in place of second deletion. → I gave the virus to Shari to grow up Cse prep.

Need Tk gene from GTI.

EXHIBIT

C36



Keroh 4/25/97

EB proteins

- I have tested more MP6K 14.7 and R1D viruses. The ones that stain for p-Gal show some staining in IF for 14.7 or 14.5. The R1D B staining shows the same pattern as the previously made ~~Ad~~ Ad R1D viruses. In addition to this, the cells that stain are dead ~~for~~ (carryover from 293?). The 14.7 staining looks normal. I am growing up more of the positive clones.

-FasL project

- I have two transfections going in 293 Com A.

Cancer Therapy project

- I have infected MCF-7 with 01/07, 975 and 308. Will do the same with A549 and 293 and take a growth curve.
- I am infecting W138 for the missing timepoints.
- I am filtering the remaining samples.

EXHIBIT

C37



1101/1107

175

308

A

G

A

G

A

G

D1

D3

D5

D7

D10

D15

D20

D25

D30

 $< 10^5$ 2×10^5 $< 10^5$ 1×10^5 5×10^5 3×10^5 4×10^5 $< 10^5$ 8×10^5 2.3×10^6 7×10^5 1×10^5 1.5×10^5 1×10^6 2×10^5 8×10^5 7×10^5 4×10^5 3×10^5 1.4×10^7 1×10^6 1×10^6 3×10^6 1×10^7 6×10^7 2×10^7 $< 10^5$ 2×10^7 4×10^7 22-141 30 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

EXHIBIT

C38

Sheet1 Chart 2

Approximate titers in WI38 4/25/97

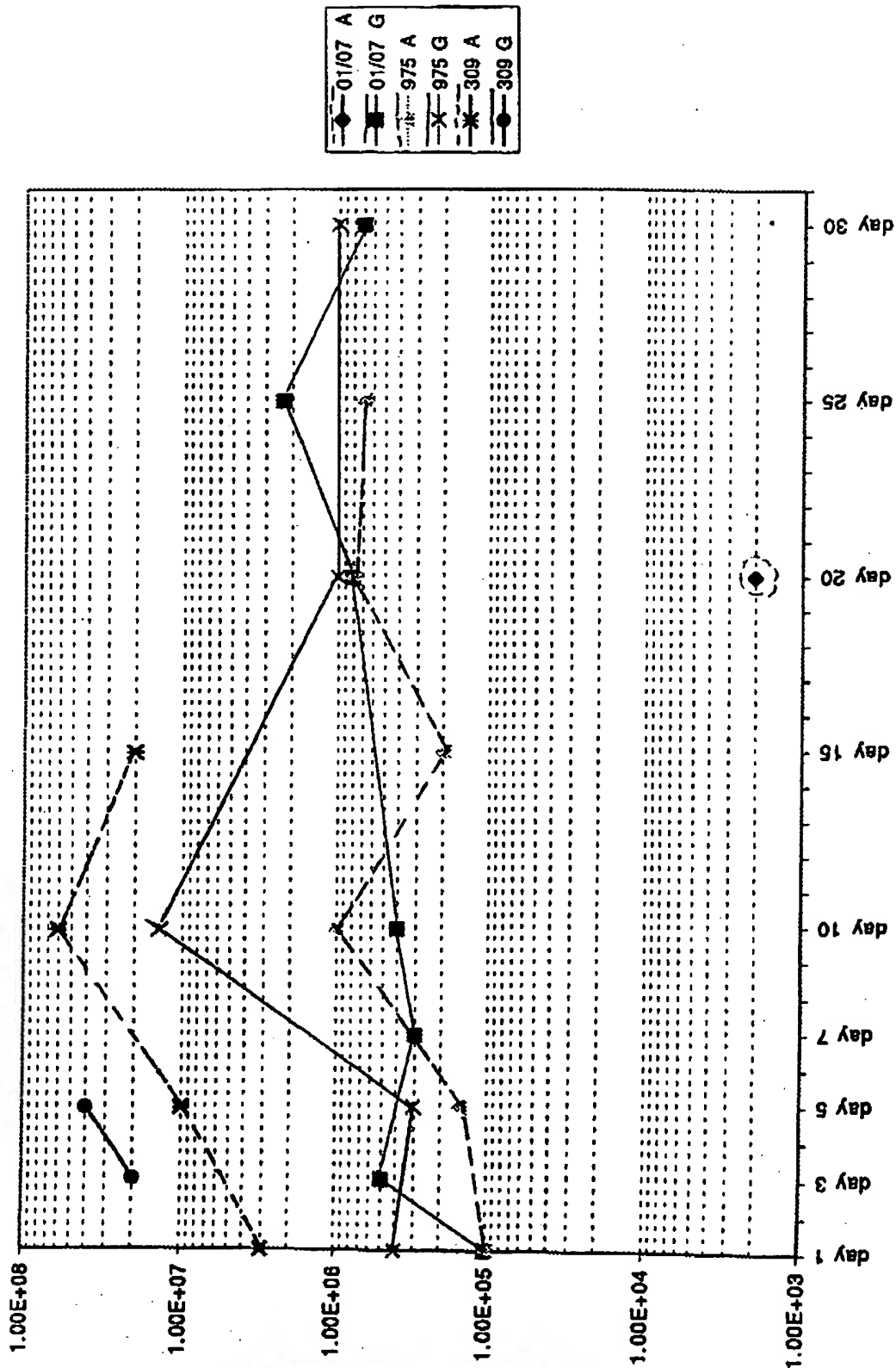


EXHIBIT
C39

Mohan, t/25/97

1 C.F. Project:

- a) cells showed CPE like effect (co-transfected pAE1SP1A/3.7SPC Rep78 and pBKG10) were titrated. No plaques yet ~15th day. But when 293 cells infected with CPE, CPE like started look Ad CPE typical.
- b) In 293 Rep78 AS - cell line, co-transfections of pAE1SP1A/3.7SPC Rep78 and pBKG10 were done; pAE1SP1A/3.7SPC Rep78 and pBKG10E3 plasmids.
- c) Virus Ct 19.7 are growing in KB MMTV E1 Spin cells.
- d) GAPDH (Glyceraldehyde 3Phosphate dehydrogenase) primers - ordered.
- e) pBKG10, pBKG10E3 under preparation for further transfections.
- f) I am going to isolate A17001 DNA for transfection → Virus Rep78.

2 Cancer Project: HEC 299 cells

Growing and Growth arrested cells are frozen for growth Curve analysis.

EXHIBIT

C 40

9/2/97 Kostya

1) Terry's gp19K plasmids: pCR11gp19K Ad5 turned out to be pCR11gp19K Ad2.

pC1gp19K contains gp19K Ad2 in correct orientation. (Karol - Transfection - IP).

2) Cloning of the complete E3 under CMV promoter;

i) There was E3 inton in Horowitz's virus, their construct starts ~200 bp after E3 transcription start in Ad2 E3.

ii) Started to extract Rec 700 and pm 734.1 (m1m41) genomes to clone E3 to pCDNA3 (or pC1?).

3) Cloning experiments to replace ITR in SP-B ↔ E4 promoter plasmid are in progress.

4) Got the virus 1101/1107 E1, ^{grows much better than dl7001} dlE3 X68 + ADP. Checked with restriction digestion and PCR. Recently started experiment (plaque assay) to compare growth properties of 3 recombinants

(Lynda's deletion E3 + ADP; ^{KD1} dl309 gp19K ^{KD2} untagged; ^{KD3} dlE3 X68 + ADP). Using dl309; 1101/1107;

pm 734.1 (m1m41); 7001 as controls. Cell lines - 293 and A549.

Going to start with IP to check for ADP expression. I'm really ready to put TK into 2 best recombinants E3, need TK plasmid and TK sequence from GT1.

Need TK from GT1!

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



Kashy 5/2/87

E3 proteins

- I am growing up NPGK 14.7 #5 showed best IF.
- I did an IP with transfected p13k and 14.7 constructs (in 293 cells). All but pCBNA3 14.7 expressed, all comparable to virus injection. (Labeling 38h post IF and 18h p.i. for 3h)
- I did an IF with the same transfections (in MCF7 cells) it did not work, I am repeating it.

LacZ-PGK-14.7k
Molten got, and not
band.

FasL project

- I am waiting for plaques in 293-Crnt cells.
Have one plaque after 10 days.

Cancer Therapy project

I have infected	MCF7	01/07 500 phn	975 100 phn	309 100 phn
	A548	500 phn	500 phn	500 phn
	293	500 phn	100 phn	100 phn

293 is rounded up 1 day p.i.
A548 2 days p.i.
MCF7 5 days p.i.

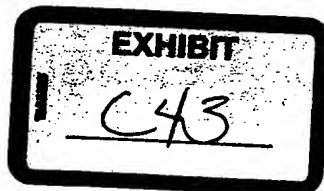
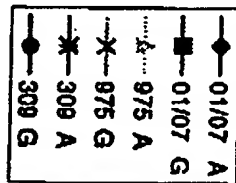
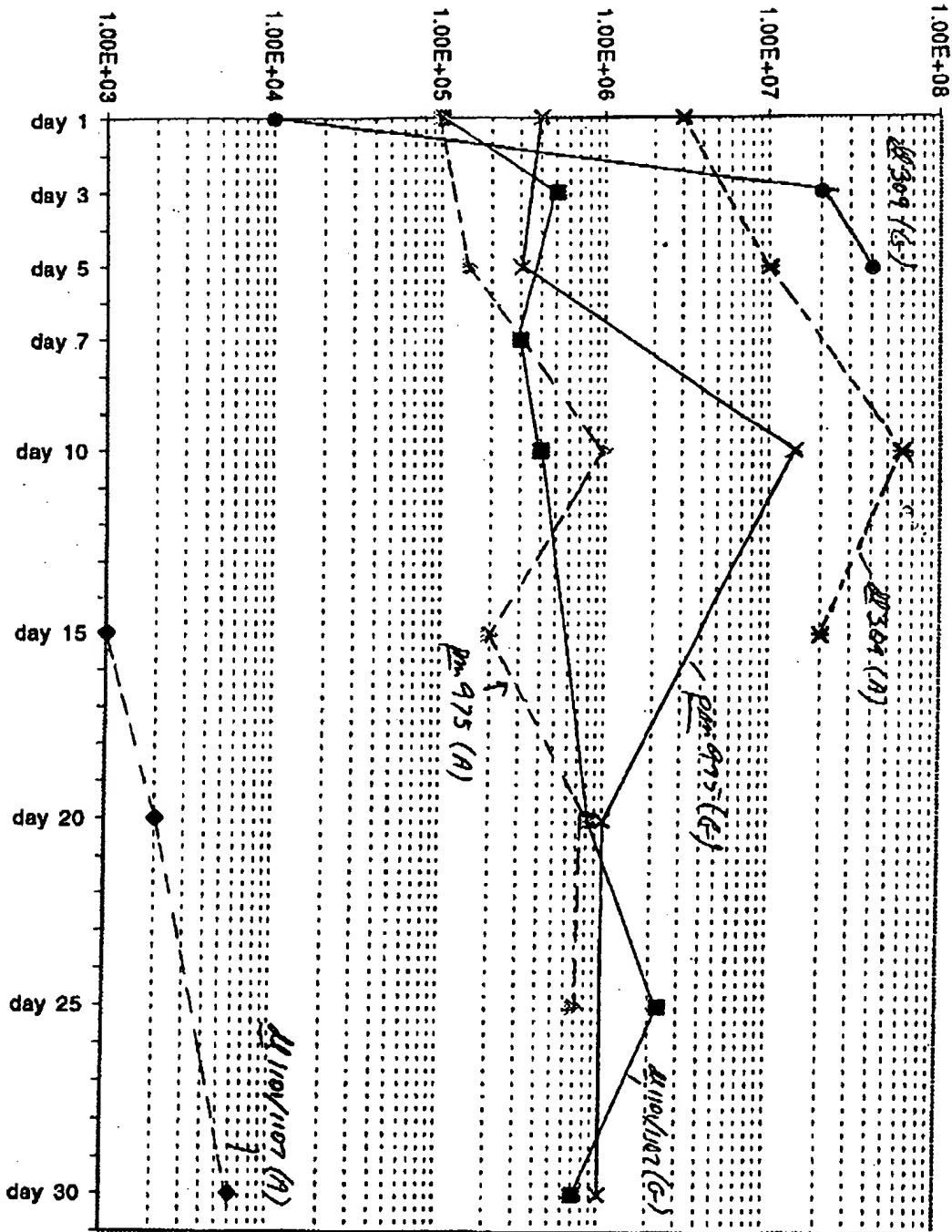
EXHIBIT

C42



Sheet1 Chart 2

Approximate titers in W138



5/2/97 Kostya

- 1) Terry's gp19K plasmids. pCR11gp19K Ad5 turned out to be pCR11gp19K Ad2. pC1gp19K contains gp19K Ad2 in correct orientation. (Karol - Transfection - IP).
- 2) Cloning of the complete E3 under CMV promoter:
 - i) There was E3 inton in Horowitz's virus, their construct starts ~200 bp after E3 transcription start in Ad2 E3.
 - ii) Started to extract Rc 700 and pm 734.1 (m1m41, genomes to clone E3 to pCDNAs (or pC1?).
- 3) Cloning experiments to replace ITR in SP-B ↔ E4 promoter plasmid are in progress.
- 4) Got the virus 1101/1107 E1; ^{grows much better than dl7001} dlE3 X6a + ADP - Checked with restriction digestion and PCR. Recently started experiment (plaque assay) to compare growth properties of 3 recombinants (Lynda's deletion E3 + ADP; dl309 gp19K unmutated; dlE3 X6a + ADP). Using dl309; 1101/1107; pm 734.1 (m1m41); 7001 as controls. Cell lines - 293 and A549. Going to start with IP to check for ADP expression. I'm really ready to put TK into 2 best recombinants E3, need TK plasmid and TK sequence from GT1. Need TK from GT5!

50 SHEETS
22-141
22-142 100 SHEETS
22-144 200 SHEETS



1. C.F. Project:

- a) BMCE3172 LacZ virus gave moderate band in CseI banding. But the β gal activity/ml is $\sim 1.4 \times 10^9$ which is same as previous IT2 LacZ preparation. Second set is being titrated to compare the pfu/Lfu/ml.

[I may use Centricon 100 (M.Wt cut off 100,000) to concentrate the viral stocks for one CseI spinning which will increase the pfu. Dialysis of stock IT2 LacZ virus will increase the volume and it is hard to spin in one tube.

- b) Co-transfection of pE1Sp1A/3.7 Src Rep78 & pB2610; pB26E3 in 293 Rep78 antisense cell line will be stained next week.

2. E3 project:

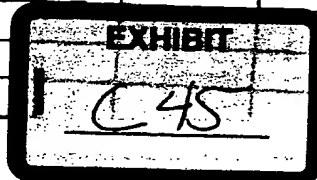
- a) Virus C+14.7 (pCKII 14.7 + p_{gluc}) gave moderate band in CseI spinning. Viral titrations are in progress.

- b) Going to make another virus 14.7 LacZ (pCK 14.7 in E3; lacZ in E1) preparation. - infection today

3. Cancer Project:

Growing and growth arrested virus infected HEL 293 cell ~~extract~~ extract will be titrated for growth curve next week.

12110/1107 at 500 PFU/cell
12309 " " "



Sheet1 Chart 3

Growth curve 3

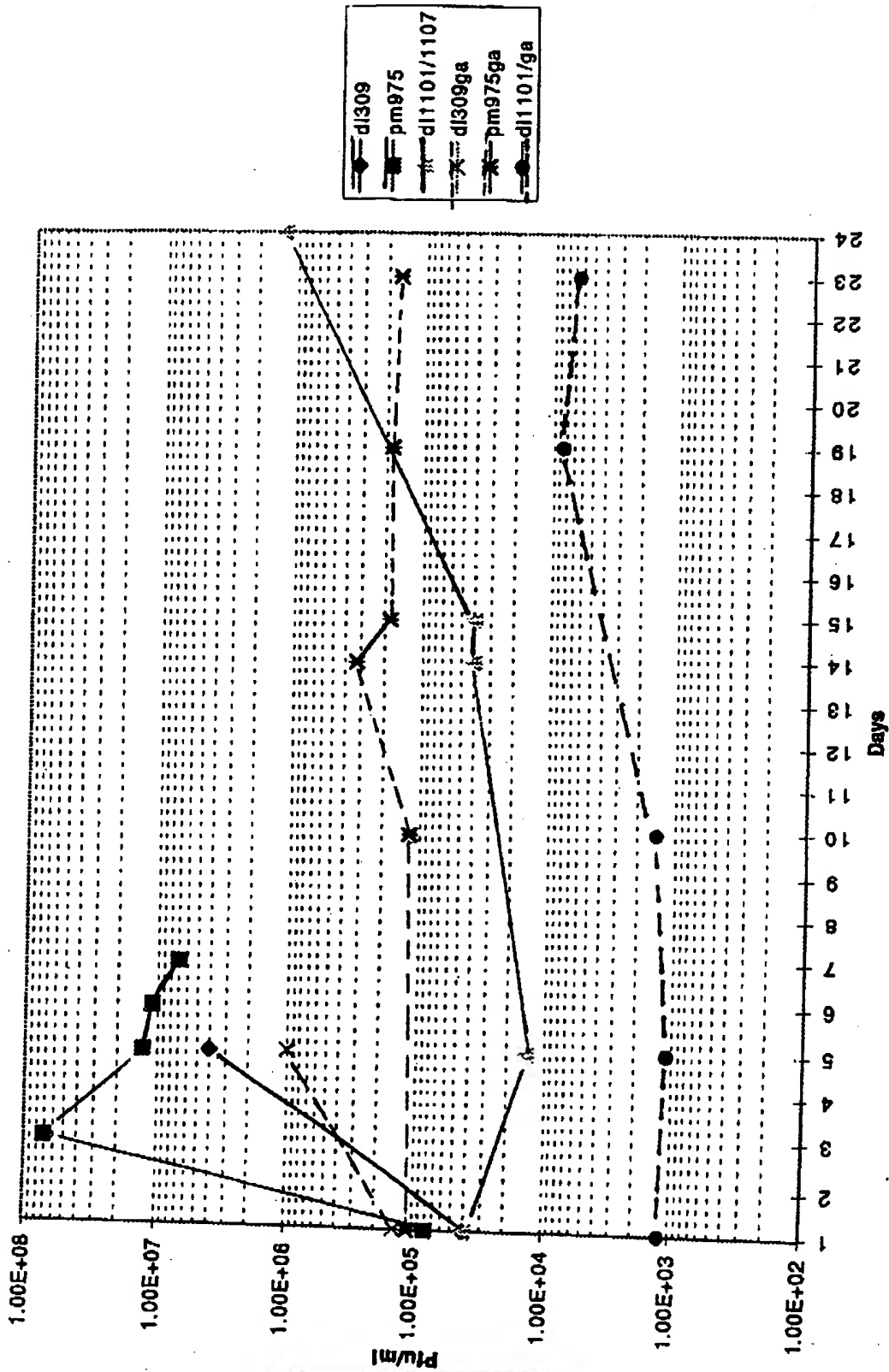


EXHIBIT
C 46

Kostya

- i) Results of cotransfection 1101/1107 /EcoRI + p54 (dLE3 + ADP) → 4 more plaques were analyzed. 3 of them contain recombinant genomes.
- ii) Subcloning of dLE309 E3 with gp19K mutated and dLE3 Xba + ADP into Linde's plasmid is in progress. When the plasmid with 19K* is made I'm going to insert HSV-1 TK into PacI site created in gp19K gene.
- ii) i) No plaques with pG2B (pBAG11 E4 promoter → CMV promoter). No plaques with pBAG11 as a control.
- ii) 4 more plaques resulting 1101/1107 /EcoRI + p82 (E4 → SP-B promoter) were analyzed. All contain wt genomes.
- iii) In 2 repetitions of cotransfection 1101/1107 with p82 (E4 → SP-B promoter) no plaques neither in control nor in experiment. 2nd experiment was done on Moken's 293/CMV-TTF cells. Now repeating the cotransfection.
- iv) Sequencing of Nipper's plasmid p21 (E4 promoter dLE) is in progress to prove that right Ad ITR is intact in the plasmid.
- i) Growing initial stocks of the recombinant virus with dLE3 + ADP.



Gene Therapy Group

Karoly 5/8/97

E3 proteins

- I am growing up MP6k 14.7 #5
 - I did an IF with transjected p13k and 14.7 constructs in MCF7 cells, all of them but pCDNA3 14.7 expressed well.
- Virus - MP6k p13k and pGlc 14.7 were negative after 20h.
Mohan is doing a large infection assay

First project

- I have 4 plaques. They appeared ^{10-11 days} after transfection with BHK21 in 293 Crm A cells. Will pick one plaque (large) today.

Cancer Therapy project.

293, MCF7, lost time mistake: Multistep Repeat: 3rd A49.

I am repeating A548 infections and some U138 infections.

CPE in U138 cells

A = 0.2% serum FCS
G = 5% FCS

01/07 A

no CPE

01/07 G

"atypical CPE" starting around day 10

No CPE in 1101/1107, either in growing or non-growing.

500 pfu

The "growing" don't really grow. But, have fewer cells in the growing than non-growing.

975 G

No real diff. between G and A for 975 500 PFU

975 A

D2 +/-
D3 +/-
D4 +
D5 ++
D6 ++

D4 +/-
D5 +
D6 ++
D7 ++

500 pfu

For 100 PFU, growing was same as 500 PFU. But, arrested did not show CPE until ~ 15 days. Same in HEL-299.

308 G

D3 +/-
D4 +
D5 ++
D6 ++

308 A

D5 +
D6 +
D7 +

100 pfu

also pCE Bay pCDNA3.1. Clone 9p19, 14.7, RLD

EXHIBIT

C48

ie photograph as done with 0 PFU.

lost plaque A - cat in test for free CPE 975, HEL-299

missing review of cell types.

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



5/9/97 Kostya

- 1) Construction of the plasmids with whole E3 (rec 700, pm 734.1) is in progress.
- 2) I have constructed the plasmid with E4 \leftrightarrow SP-3 where T_uS \leftrightarrow ITR, sequenced the plasmid, now waiting for sequencing results to make the large version of the plasmid for cotransfection.
- 3) For 101-1 (dl 3.9 E3, gp 19K untested) plaques are appearing the same day as for 309 (day 4).
For 111-1 (E3 XbaI dl + ADP) plaques appeared 1 day before dl 309. (day 3)

① KD-1. 1101/1107 in Lynda's E3 background + ADP.
No promoter for ADP.
Shari harvested day 2 pi, got band, will titer.
Cells were beginning to die. Shari will titer.

② KD-2 1101/1107, 309 E3, gp 19K untested.
Plaques appearing same day as 309.

③ KD-3 1101/1107, XbaI deletion (dl 327 deletion),
ADP without promoter, but in-frame = 6.7K.
Got plaques 1 day before dl 309 (ix on day 3).
Got this ^{one} plaque 4 days posttransfection, 5mm wide.
Got other 3 plaques 7 days posttransfect
DNA screened - are recombinant.

Future - could put ADP under control of SPB promoter.
First, concentrate on what we have.

infected ADP with 29.3 cells



Mohan, 5/9/97

1. C.F. Project:

- a) Virus BM6 E3 ITR LacZ gene 1.4×10^9 Lfu/ml (preparatory)
 Plaque assay gave 9×10^8 pfu/ml (10th day)

I received Centricon 50 concentrator from Millipore as
 Samples - going to concentrate the ITR LacZ virus.

- b) So far no plaques for constructing Rep78 virus.

- c) GAPDH - RT-PCR in progress.

- d) Going to G-transfect d1700 DNA (lat digested, with
 pSPC Rep78 plasmid).

2. E3 project:

Distinct conversion, left-to-right orientation

- a) Virus C+14.7 (p^{pol II} 14.7 + p^{gluc}) has been
 Titrated. No plaques yet - 10th day.

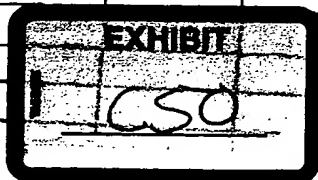
- b) CPE stock for 14.7 LacZ (p^{pol II} 14.7 + LacZ) virus
 has been made. Going to titrate (5ml final)

- c) A549 cells are infected \pm 1700, GP19K and
 C+14.7 virus for i.f. (2 days & 4 days)
 Hard 2 days - negative already infected.

3. Cancer project:- HEL 293 cells

Growing, growth arrested, d11/01/07 (Graph
 infected - CPE stocks are Titrated for growth curve
 Will do 3rd in coming week)

HEL-293 100, 500 PFU Graph: days p.i vs CPE - will give more.



5/23/97 Kostya

1) E3 project:

Cloning of E3 from rec 700 and pm 734.1
in pBSSK (+) - got bacterial colonies, cycling,
then reclone into pCE, then make virus.

2) Cancer therapy project:

- i) Made a large plasmid (Bom → end of genome)
with E4 → SRB promoter and ITR repaired,
now making Cae prep. of the plasmid to transfect.

Next week make virus

- ii) Plaque development assay for E3 ADP viruses:

a) 293 cells (day 18)

Negative control:

7001 - plaques just started to appear (day 18).

734.1 - plaques appeared day 14-15

Positive control:

309 - day 4-5

1101/1107 - day 4-5

Recombinant viruses:

KD1 (544, LKH d1 E3 + ADP) - day 5-6, plaques smaller than wt.

KD2 (101-1, d1309, gp 19K *) - day 4-5, large plaques.

KD3 (111-1, d1327 + ADP) - day 4-5, large plaques.

b) A549 cells (day 8)

Same day a little faster than wt
Perhaps a little larger.

309 - day 4-5 (large)

1101/1107 - day 8 (small)

734.1; 7001 - no plaques yet.

KD1 - didn't make

KD2 - day 5-6, large, smaller than wt. (309)

KD3 - day 5-6, smaller than KD2.

positive
control

negative
control

rects.




Mohan, 5/23/97

1. C.F. Project:

- VIRUS BHGE3 ITR LACZ WAS CONCENTRATED USING CENTRIFUGAL FILTER COLUMNS. Lfu is $\sim 3.86 \times 10^{10}$ /ml. (cal ml)
- d1700⁺ VIRAL DNA DIGESTED WITH *clai* AND pAE1sp1A/SPC10P1 WERE CO-TRANSFECTED.
- 293 TTF CELL LINES WERE TRANSFECTED WITH pAE1/SPC10P1. I.F. STAINED FOR REP78. MOST OF CELLS TRANSFECTED WITH pAE1/SPC10P1 WERE WASHED OUT. FEW CELLS (ABOUT 3) SHOWED NUCLEAR STAINING. BUT NOT CLEAR.
- 293 L⁺ REP78 ANTISENSE CELL LINES SHOWED GAPDH-PCR FRAGMENT NOT THE REP78 FRAGMENT. SO, NO AA VZ CONTAMINATION.

2. E3 Project:

- NP6K LACZ 14.7 (CPE STAIN) $\text{gand} = 3 \times 10^8$ Lfu/ml in 293 cells
but in A549 = 2.3×10^8 Lfu/ml. ~ 10 fold more in A549 cells than 293 cells.

- I.F. = A549 cells: T700 - 21 hrs (21 hrs) + + + + for 14.7
 ~ 50 pfu/cell NP6K 14.7 - 1 day -
2 day -
(Bacteriophage columnar) 4 day + + + +
- 4 day + + (cytoplasmic staining)
GP19K = Background 

VIRUSES NP6K 14.7 EXPRESSES 14.7 AT 4 DAYS POST INFECTION AT WT. LEVEL.

Ct 14.7, at 4th day expresses lesser. Mainly cytoplasmic staining and around the nucleus.

Ct 14.7 when titrated $10^7, 10^8, 10^9$ no plaques. - Titer may be less. So, -IF- may be less.

EXHIBIT

CS2

3 Cancer project: HZL 299 cells 500 pfa/cell

Growing

d1309 d1401/07

3 hrs	9×10^3	2×10^4
1 day	1×10^4	4.2×10^4
4 "	1.6×10^4	1.2×10^5
6 "	2.3×10^4	
8 "	9×10^6	1.4×10^5
10 "		7.1×10^5
15 "		2.2×10^6
21 "		4.6×10^6

Growth arrested

3 hrs	4×10^4
1 day	4.4×10^4
4 "	4×10^4
8 "	5×10^4
10 "	1×10^4
15 "	1×10^4
21 "	2×10^4

EXHIBIT

CS3

Landy 5/23/97

ES proteins

- I am doing an IP with NPGK 14.7 and Ct 14.7
- I am growing up lac-Pol II p19K
- I am cloning the MT2 expression cassette in pC12Pac (Lynda changed the BamHI and BpI sites to PacI in pC1)

Fas L project

- I have isolated 4 plaques. ^{Could be WT.} They grow very fast (kill 293 ON, show CPE in A549 ON).
I have infected MCF7 and MCF7crmA cells, it shows CPE ON in both.
- I have tried to PCR out Fas L from the virus, it failed. Positive control (plasmid) was OK.
- The virus expresses β -gal
- I am trying to show the protein in IF.

Cancer therapy project

- I am going to titer yields from A549, MCF7 and 293 next week.

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

5/30/97 Kostya

1) E3 project :

Made the plasmid with E3 from pm 734.1 (u1u41).
(ADD⁻) - Sfi1-Xba1 - fragment in pBlueScript. Now cloning
is in progress to put it into pCDNA3.1zeo(+)- new
plasmid with CMV promoter. Now just started

2) Cancer therapy project :

i) Made cotransfection of 1101/1107 / EcoRI with ^{Bam → mp100} p152^{SPB}
(new version of large plasmid Bam - ~~end~~ with ⁱⁿ ~~ET~~ ^{ET}
SPB → E4 promoter substitution). to 293 and promote
293-TTC cells, cotransfected pCMV/TTC as well. Has ITR
(made by Nohan)

ii) Plaque development assay for E3 ADP viruses :

293 cells - see graph.

AS49 cells - in progress.

iii) Starting IP with ADP sera to check for
ADP expression in the viruses - direct.

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

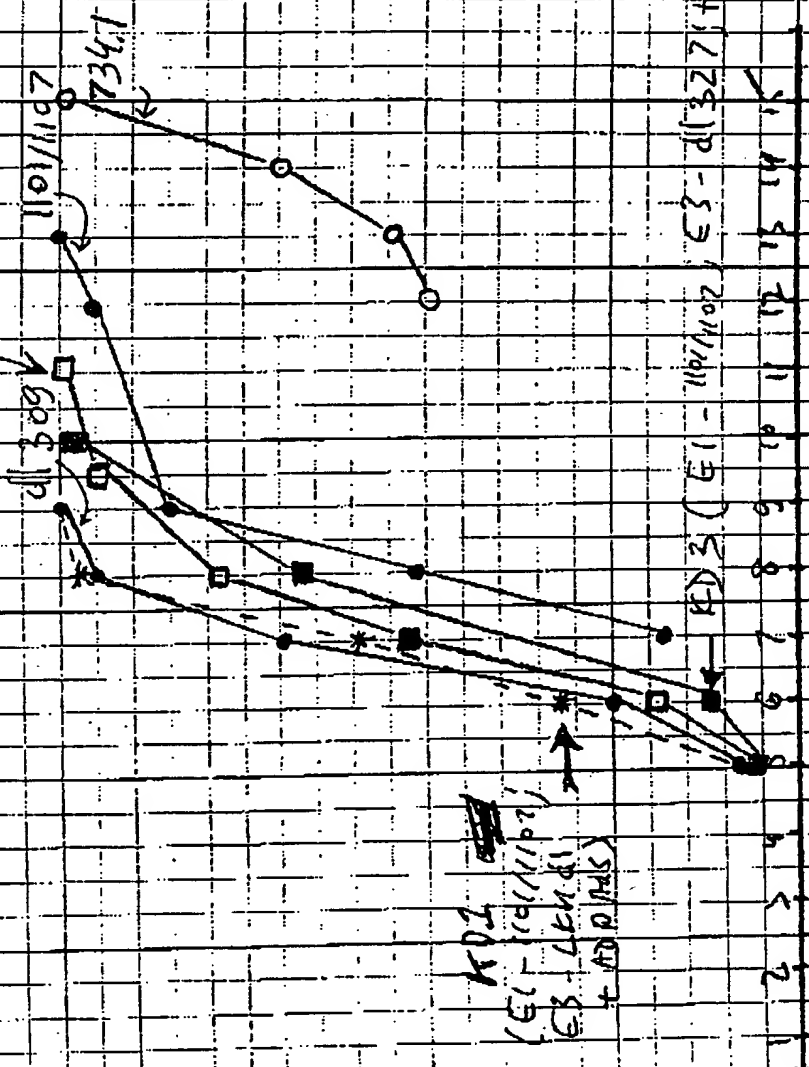


Kostyga

Plaque development assay; AS49 cells

ED 2 (E1-1101/1102; E3-d1309, sp19k*)

Percent of three plaques



Days post infection

EXHIBIT
956

Korohy 5/30/97

E3 proteins

- I did an IP with NPGK 14.7B, the result is not conclusive.
- I am repeating the MTZ cloning.

Fest project

- The tested four plaques were not expressing β -Gal. I found two bmc cells, I don't know where they came from.
- I have 3 new plaques, they came at the same time as lacZ controls.

Crm A

I am cloning CMV-CrmA in the left end plasmid

Cancer Therapy

- I am titrating the time course in A549, MCF-7 and 293 cells started yesterday.

E2-Gal

I am waiting for plaques
No plaques on lacZ control yet either.

In Chip's GAL4-TAD 293 cell line

(24 and 8 days).

BH611, E2A promoter substituted
i Gal4/TATA.

lip- give Ad2 x Ad5 combo. in pCI, to Karl. Make Ad vector \pm lacZ
- Give R572TA-14.7K, pCI-14.7K, pMT2-14.7K to Nolan. Make Ad vector \pm lacZ
- type - will handle gp19K/CMV, Ad2 version.

EXHIBIT

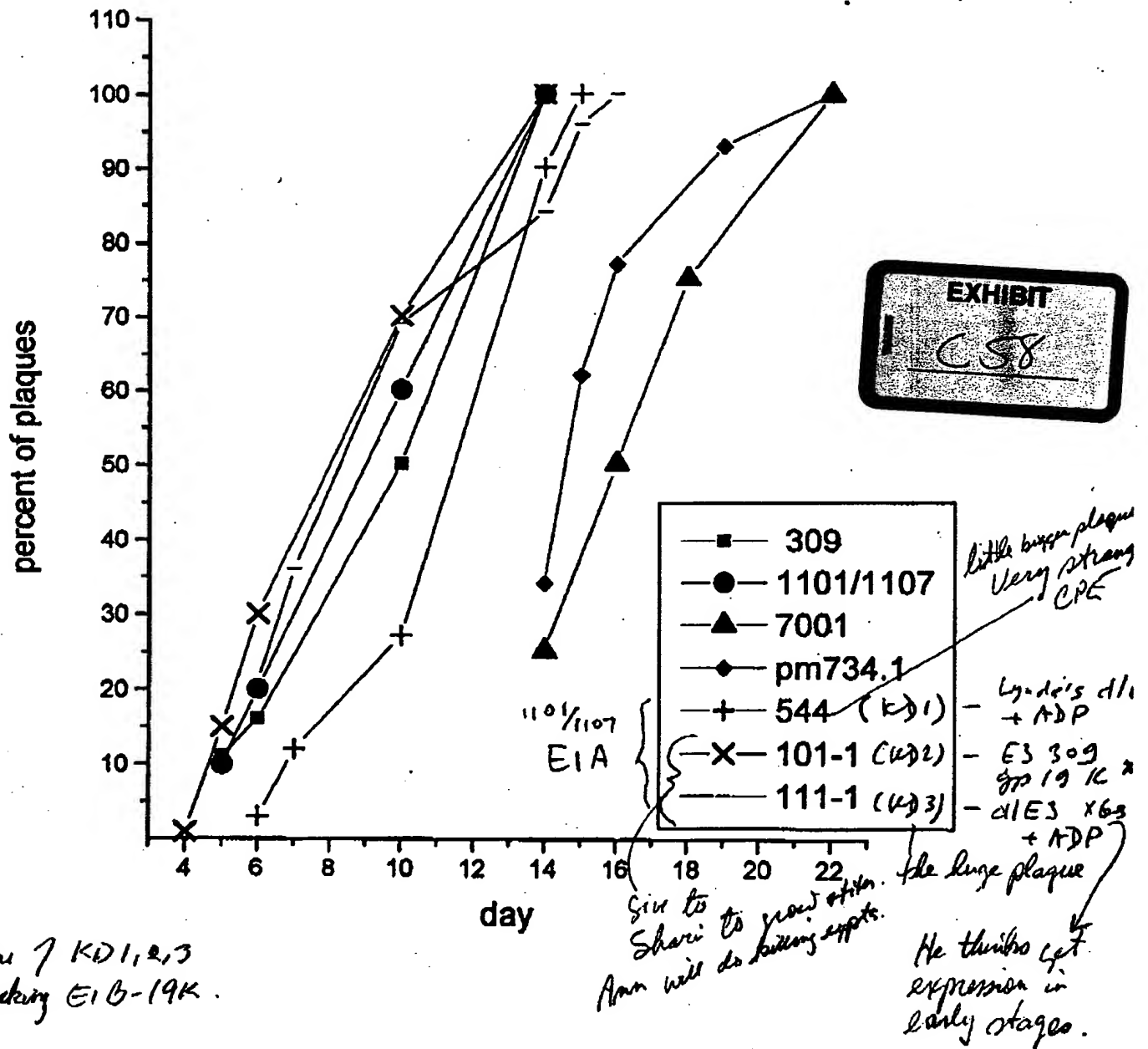
C57

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



EXHIBIT

Plaque development assay (293 cells)



Make on 7 KD1,2,3
also lacking E1B-19K.

As49 expt - now at 14 days. Look like 293, but 309 is a bit faster.
So 1101/1107 mutant does slow plaques a little.

Moham 5/30/97

1. C.F. Project:

- a) 293 cells (2 Rep 78), transfected by dl 7001 DNA (2⁴ started showing plaques (~40/60mm dish) ~ 15 days
- cells co-transfected with pAE1 Sp1A/3.7 SpC Rep78 and dl 7001 + ClaI digested viral DNA
 - no plaques yet. (15th day)
 - cells transfected by dl 7001 + ClaI - no plaques -

(I am going to several transfections using dl 7001 + ClaI digested DNA)

- b) MCF-7 ~~cells~~ cells were transfected - as following plasmids for I.F. for Rep78
- 1) pCDNA3 Rep78 (I.F. will show Rep78 expression)
 - 2) pCMV TTF
 - 3) pCMV TTF + pAE1 Sp1A/3.7 SpC Rep78
 - 4) pAE1 Sp1A/3.7 SpC

- c) Primers for Rep78 antisense → ordered.

2. E3 project:

- a) Viruses C+14.7 (Roastin promoter), 14.7 LacZ (p0 2 14.7)
- did not show plaques at 10⁻⁷ dilution.

particles/OP; for wt Ad 9.04 × 10¹³ / ml - STD.

		1	2	ptu	Particle/OP = OPS
Cell	r 700	0.174	0.167	9.88 × 10 ¹⁰	~ 1.54 × 10 ¹²
	C+14.7	0.232	0.217	~	~ 1.9 × 10 ¹²

CPE 90% - APGK 14.7 - 0.869 0.861

(medium is interfering)

L_{fu}
3 × 10⁸ - 293
2.3 × 10⁸ - 293

→ Going to repeat with more dilutions.

- b) After C+14.7 and 14.7 LacZ ptn → I.F.

EXHIBIT

1 C59

3. Cancer project: HEL 299 cells; 500 pfu/cell

dl309 growth arrested cells → stained
→ plaques start~~ing~~ appearing. Count on 2 day

EXHIBIT

C60

Sheet1 Chart 6

Growth curve 500 pfu/cell
(HEL 299 cells)

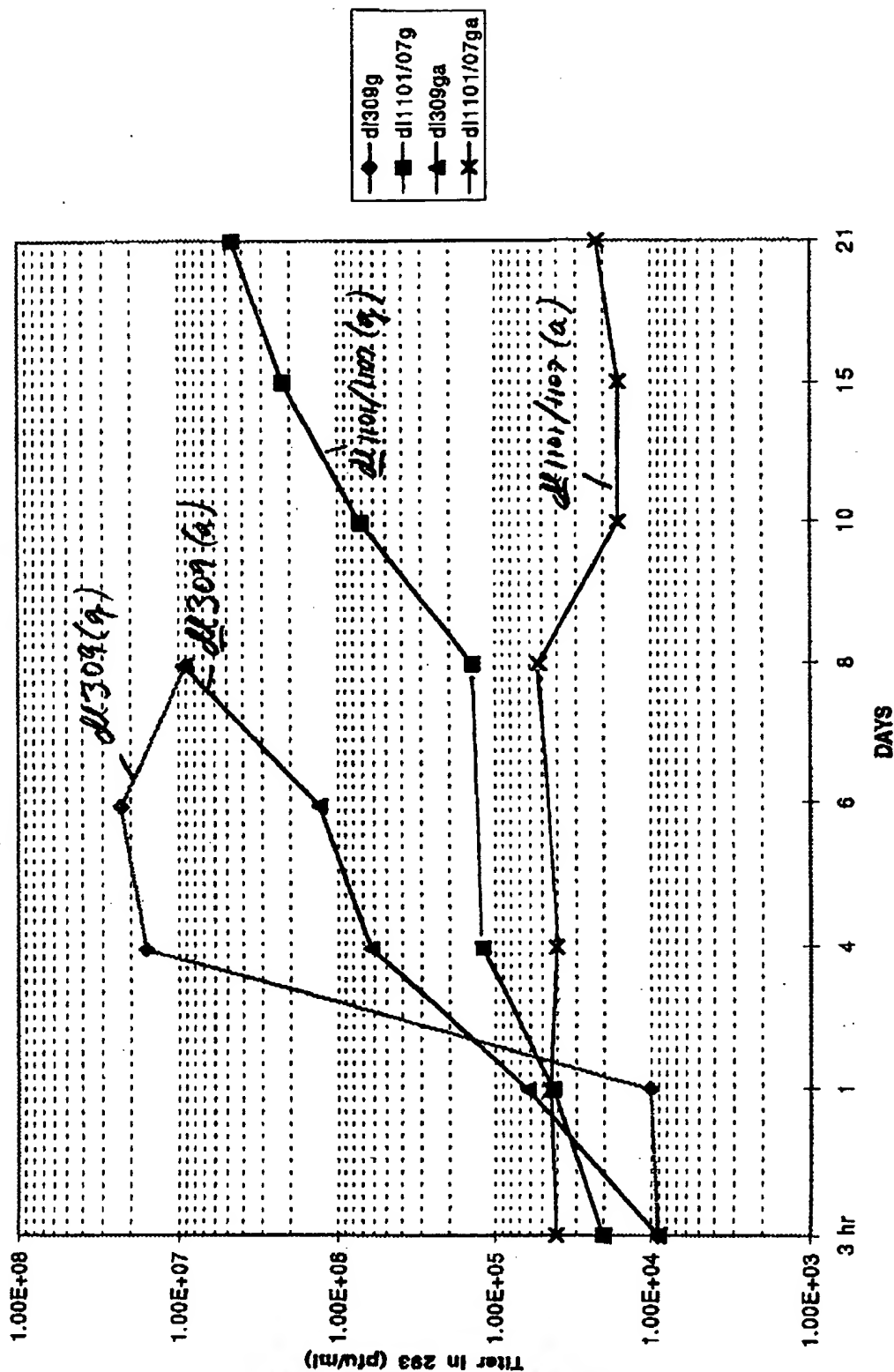
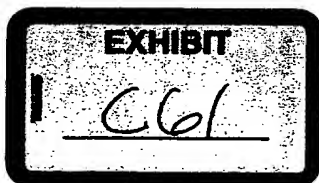
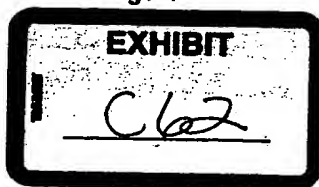
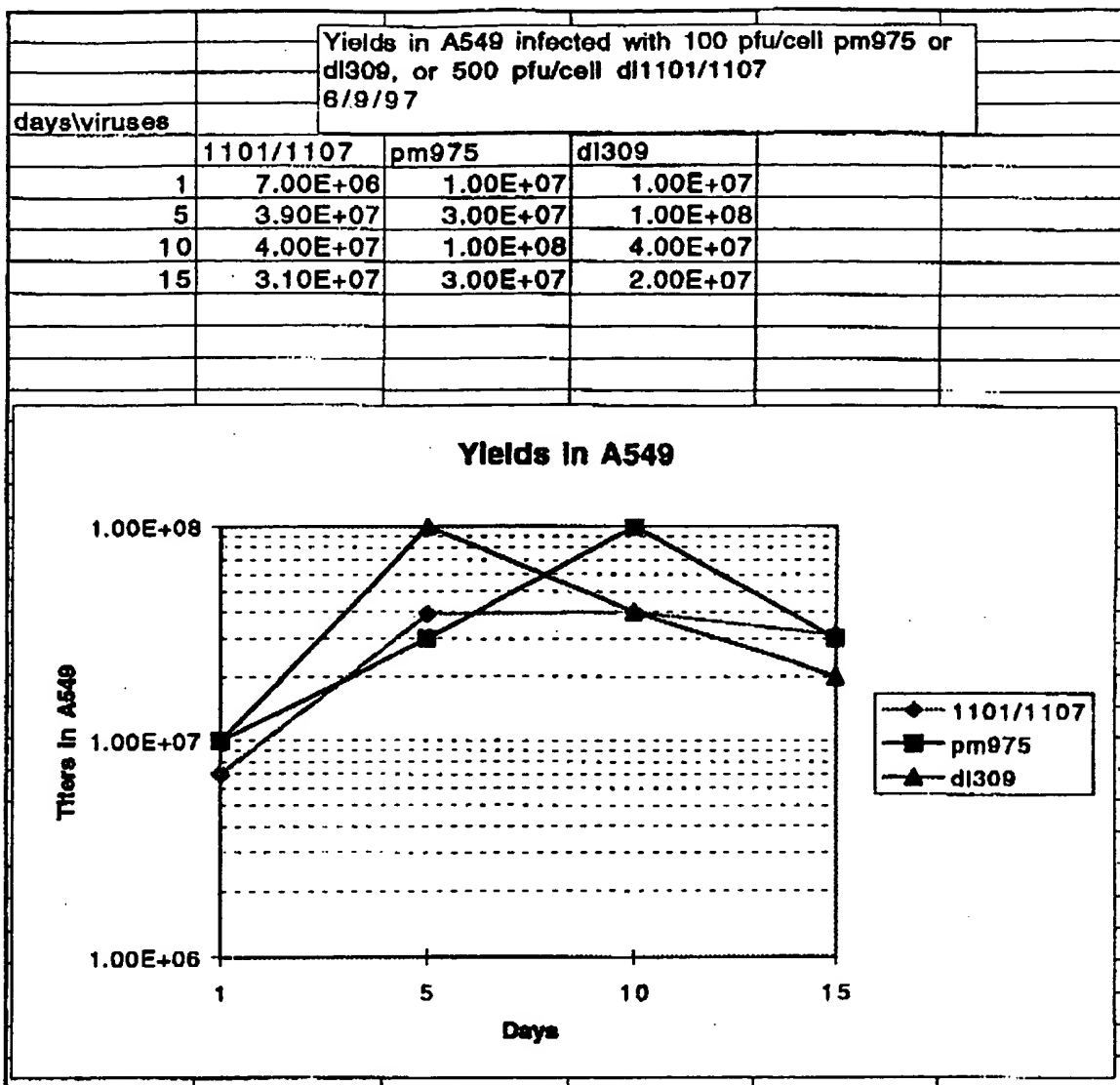


Figure 1.



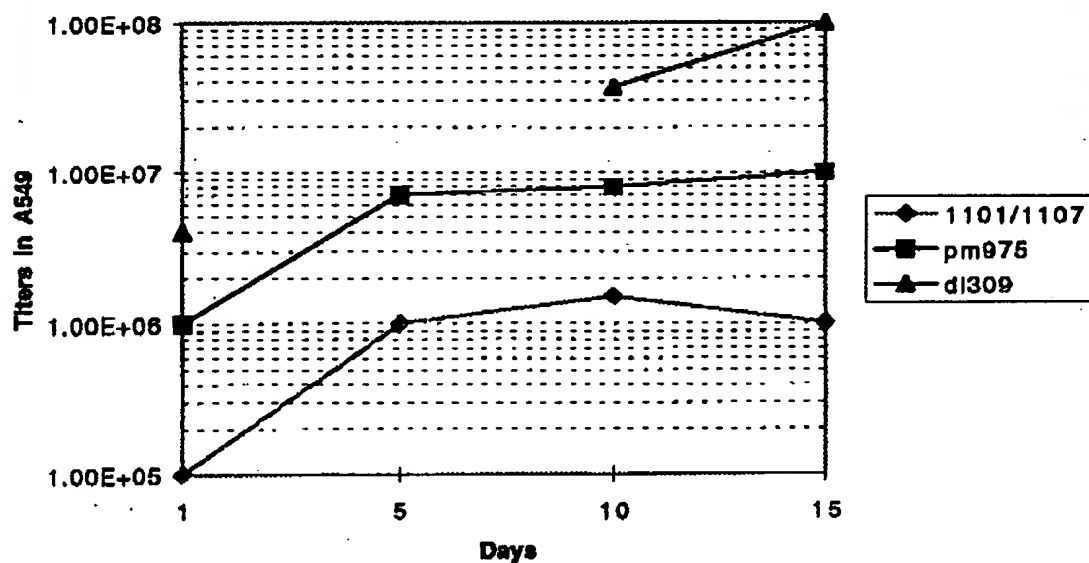
Sheet1



Sheet1

Yields in MCF-7 infected with 100 pfu/cell pm975 or dl309, or 500 pfu/cell dl1101/1107 6/9/97			
days\viruses	1101/1107	pm975	dl309
1	1.00E+05	1.00E+08	4.00E+06
5	1.00E+08	7.00E+08	
10	1.50E+08	8.00E+06	3.70E+07
15	1.00E+06	1.00E+07	1.00E+08

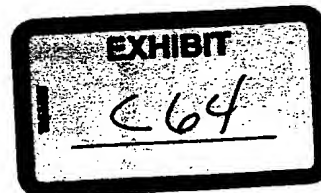
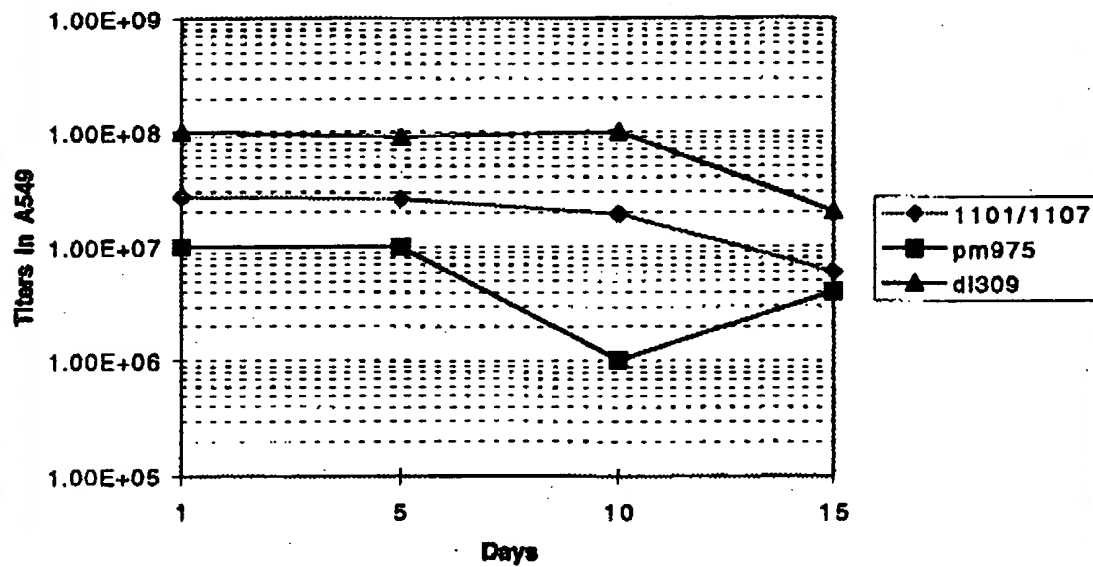
Yields in MCF-7



Sheet1

Yields in 293 infected with 100 pfu/cell pm975 or dl309, or 500 pfu/cell dl1101/1107 6/9/97			
days\viruses	1101/1107	pm975	dl309
1	2.70E+07	1.00E+07	1.00E+08
5	2.80E+07	1.00E+07	9.00E+07
10	1.90E+07	1.00E+06	1.00E+08
15	6.00E+06	4.00E+06	2.00E+07

Yields In 293



6/15/97 NOS 1/92

1) E3 project

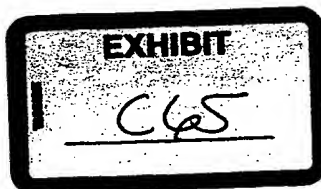
Made the plasmid with E3 (SrfI - NdeI) from pm754.1 (ADP-) in pCDNA3.1zeo(+). Gave maxiprep to Karol to check for E3 proteins.

2) Cancer therapy project

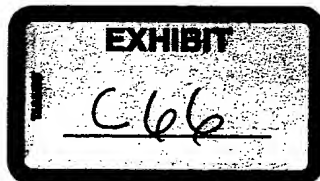
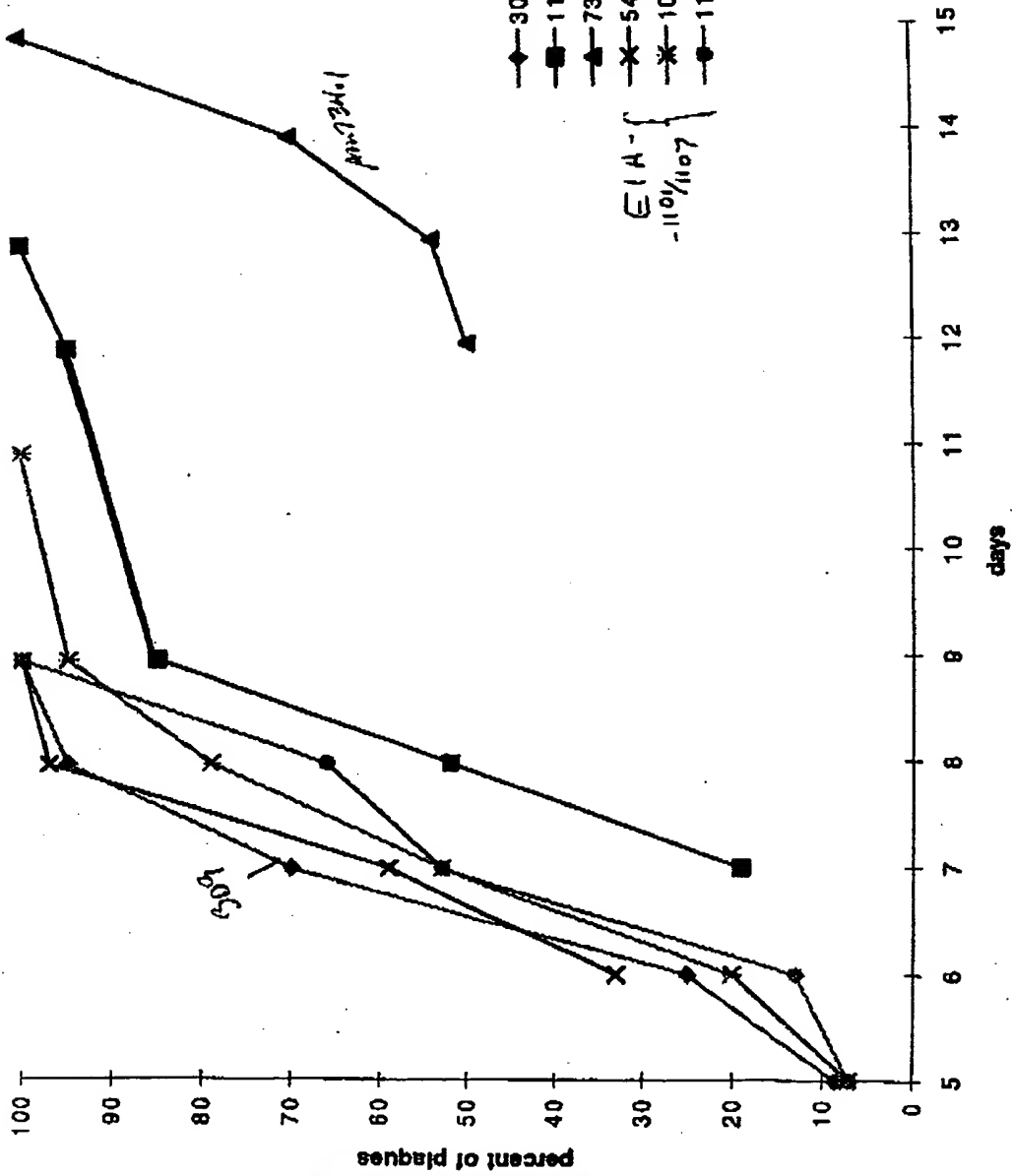
i) There are no plaques yet in dishes with p152 (E4SPB) transfection (2 weeks).

ii) Plaque development assay for E3 ADP viruses in A549 - see graph.

iii) IP with anti-ADP serum didn't work (even in positive control). Next week going to try IP with controls and various sera to optimize experiment conditions.



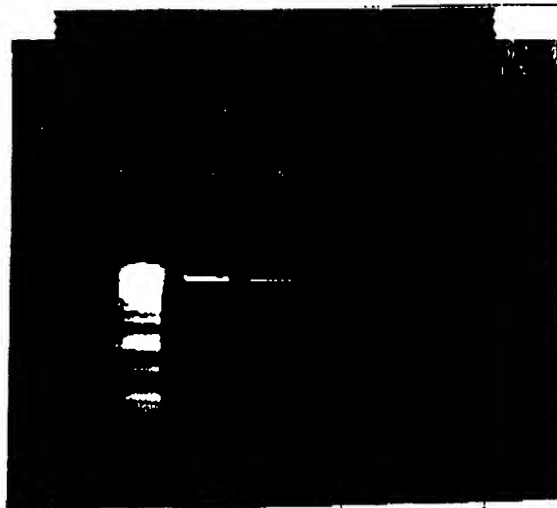
Plaque development assay, A549



Mohan, 6/13/77

1. C.F. project

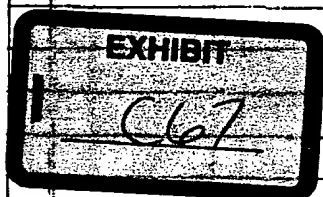
- a) 293 cells expressing anti. by p2E1Sp1A/3.7Sp1 Rep78 a viral DNA - stores the f slow.
- b) 293 Rep78 cell lines sho. fragment by PCR



2. E3 project:

a)

Particles/OD, OPU



	OPU ¹	OPU ²	Pfu
r700	1.52×10^{12}	9.5×10^{11}	9.88×10^{10}
C+14.7	1.9×10^{12}	9×10^{11}	-
GP19K	-	2.8×10^{11}	1.2×10^9
ITR LacZ	-	2.2×10^{12}	9.8×10^{10}

PFU unit be $\sim 10^3$ replicable

- b) Lact purified r700, C+14.7, and GP19K virus - 100 μ l \rightarrow viral DNA \rightarrow gel.

It seems from the gel, OPU/DNA ratio looks reasonable. ~~WR~~

If it is true then virus prepn - does it have more defective particles in C+14.7, or Toxic?

- c) I.F: A549 cells, r700, NP6K 14.7 and GP19K (50 p.p.m.) \times 14.7.

- d) Transferring GP19K fragment from pCI19K to left hand plasmid p2E1Sp1A and p230 (p2E1Sp1/NA1) #30 NP6K \rightarrow pCI. Have clone p2E1Sp1. I have a clone in p2E1Sp1A \rightarrow plasmid prepn \rightarrow I have clones in p230 vectors \rightarrow analysing. NA1, NA2, LacZ

- e) Cancer project: HEL 299 cells, d1309 and d1101/127 (50 p.p.m.) See growth curve graph

Sheet Chart 6

Growth curve 500 pfu/cell

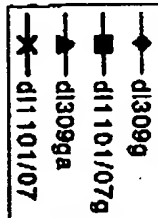
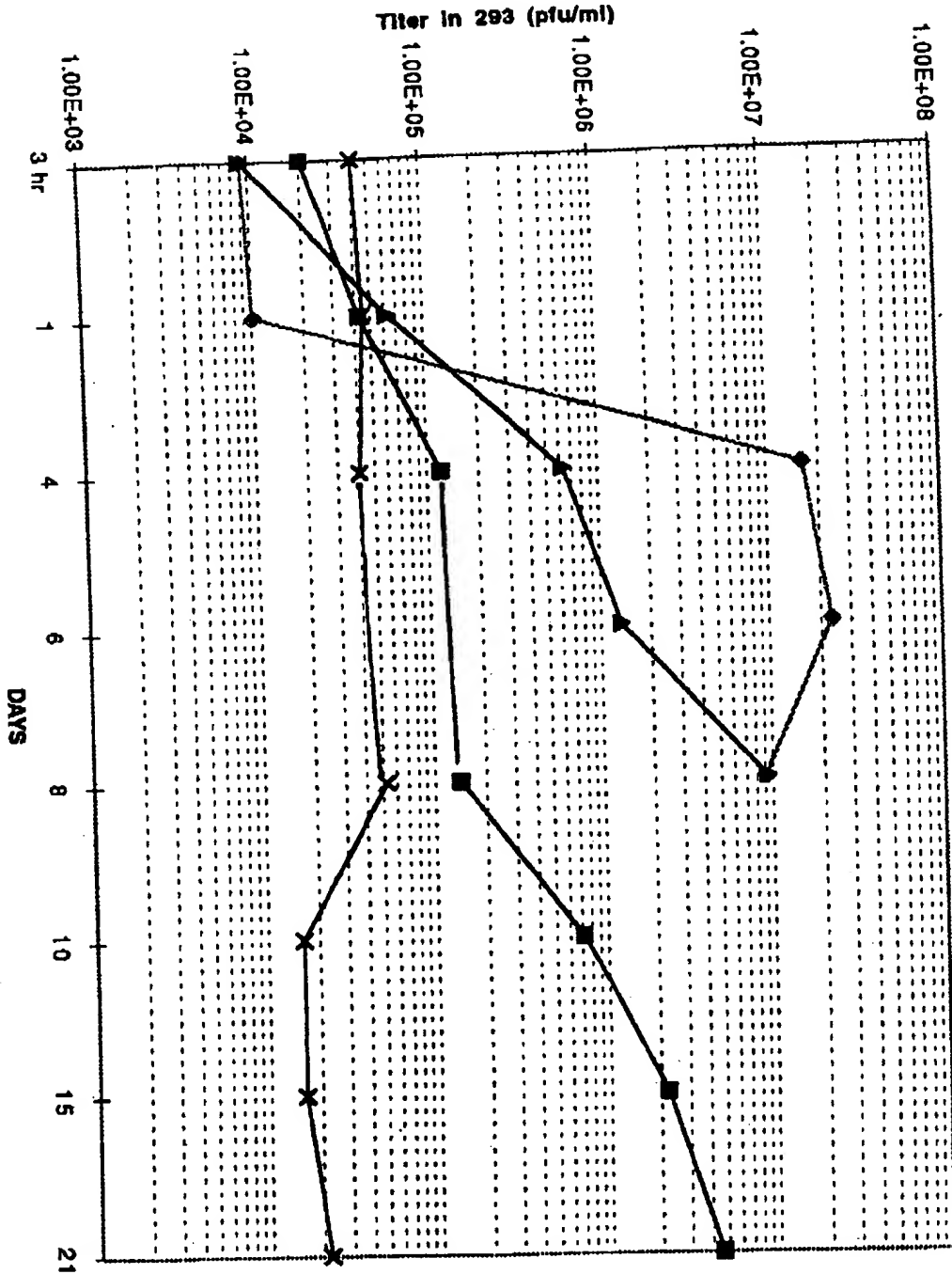


EXHIBIT
C68

KANDY 6/12/3+

E3 proteins

- I did a Western with Ct 14.7 and VP6K147B
- I am doing an IF with Kostya's CMV E3 and Todor's 760 R10
- I have a problem with cloning, I am working on it.

Fas L project

- I have ~ 15 new plaques, they came at about the same time as 12C2. I am growing them up.

Cancer Therapy

- Time course in 293, A548 and MCF 7 is done, I am making 0 hour timepoints.

E2-Gal

- No plaques yet (not even in control).

EXHIBIT

C69



Kostya 6/11/97

1) E3 project.

734.1 ← E3

i) Have made the left-hand plasmid based on p#30 (pSEISp + leez-RSV) with CMV-E3 pm 734.1 expression cassette in it. Now making cell prep. to check for expression and making virus.

ii) Failed to clone some CMV-E3 pm 734.1 into plasmid with Lynda's E3 deletion. Going to reclose CMV-E3 pm 734.1 into pCI 2Xba (Lynda), then I'll be able to put the expression cassette to PaeI site of either Lynda's plasmid or pBK611.

iii) Karol has shown that Terry's PC1/14.7 either don't express or express weak. I'm going to clone 14.7 from pMT2/14.7 to pCDNA3.1(zeo(+)), then CMV-14.7 to p#30.

2) Cancer therapy project.

i) Got 293/E4 from Valery Krougliak. Now growing them up to freeze and to repeat transfection experiments with SP-B ↔ E4 promoter substitution.

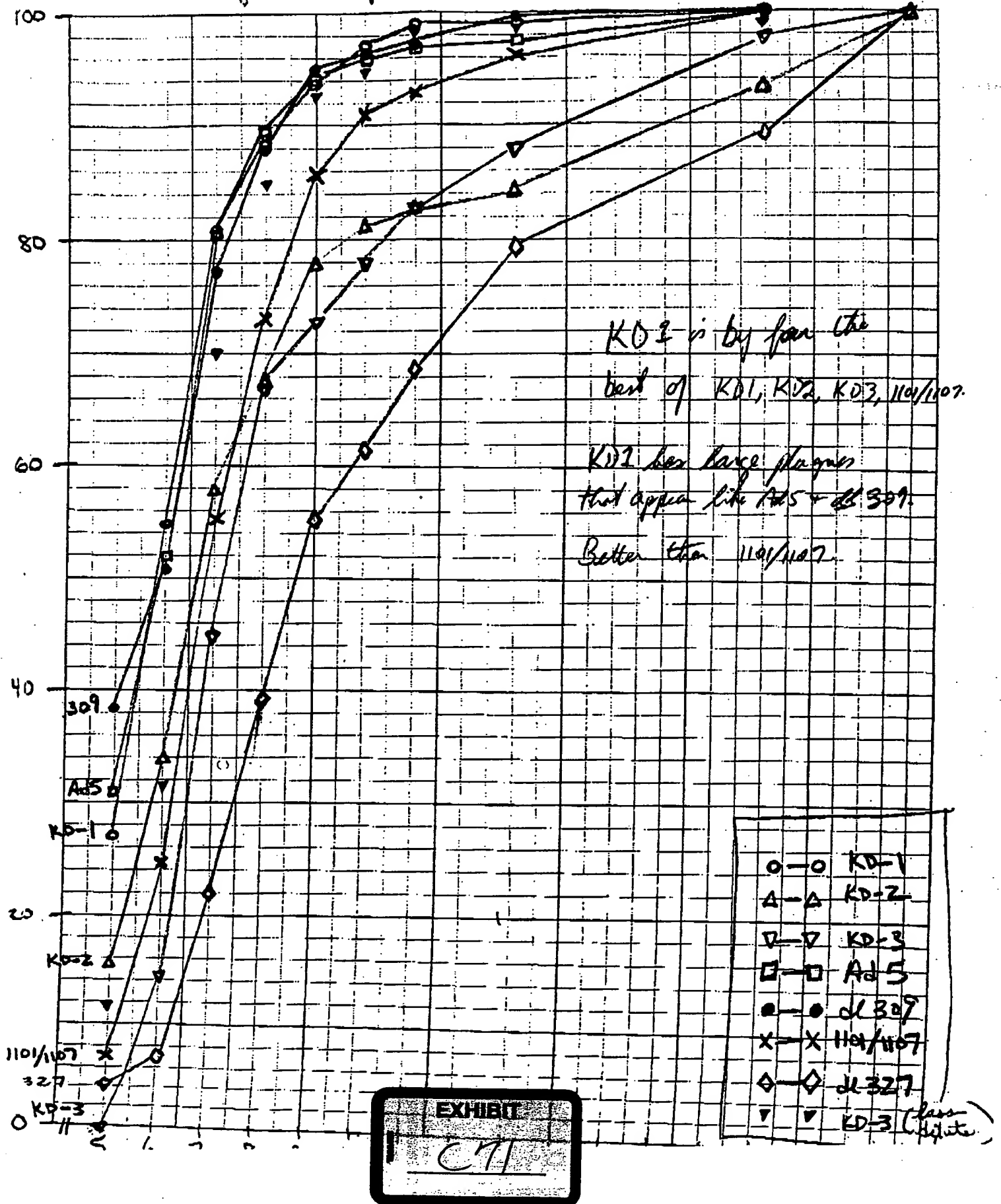
- Plaques are later than E4(+)
- Plaques are of different morphology (d1366 for me as well)
- Defect of linearization?

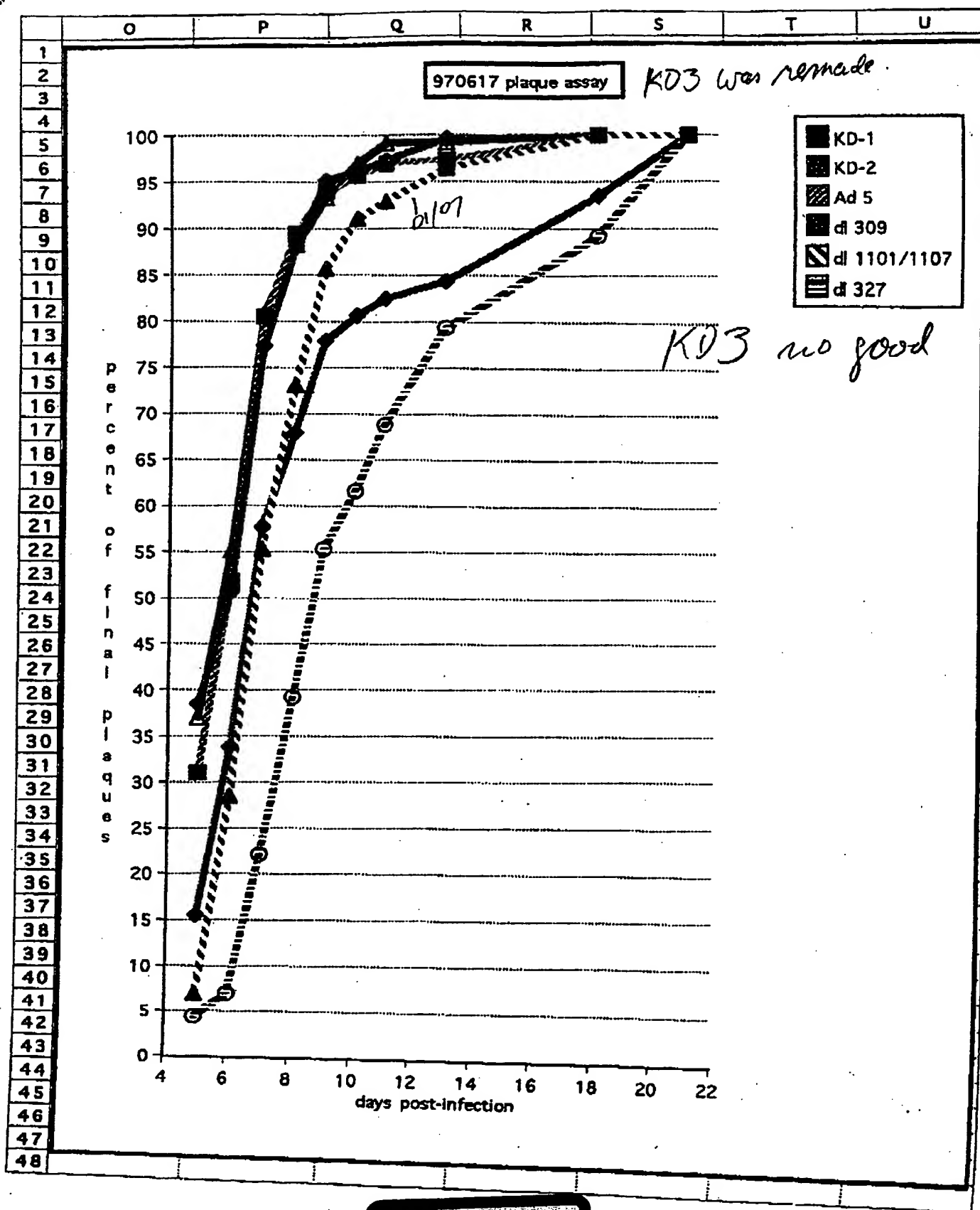
ii) 293 cotransfection of p626 E4 ↔ CMV + d1366.
293 cotransfection with E4 expressing plasmids.

iii) Ann's results with K13



970617 Plaque Assays on AS49





EXHIBIT

C72

	A	B	C	D	E	F	G
1	970617 PA						
2	KD-1	5	6	7	8	9	10
3		37	55.2	80.9	88.4	93.4	97.1
4	KD-2	5	6	7	8	9	10
5		15.6	33.9	57.8	67.9	78	80.7
6	Ad 5	5	6	7	8	9	10
7		31.2	51.9	80.6	89.5	94.1	95.8
8	dl 309	5	6	7	8	9	10
9		38.5	50.8	77.5	88.1	95.1	96.3
10	dl 1101/1107	5	6	7	8	9	10
11		7.1	28.6	55.4	73.2	85.7	91.1
12	dl 327	5	6	7	8	9	10
13		4.5	7.1	22.3	39.3	55.4	61.6
14							
15							
16							
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47							
48							

EXHIBIT

C73

	H	I	J	K	L	M	N
1							
2	11	13	18	21			
3	99.2	99.2	100	100			
4	11	13	18	21			
5	82.6	84.4	93.6	100			
6	11	13	18	21			
7	97	97.5	100	100			
8	11	13	18	21			
9	97.5	99.6	100	100			
10	11	13	18	21			
11	92.9	96.4	100	100			
12	11	13	18	21			
13	68.8	79.5	89.3	100			
14							
15							
16							
17							
18							
19							
20							
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EXHIBIT

C74

06/20/97

Hostya

1) E3 project

- i) Started cloning of CMV-E3 pm 734.1 ^{has zeocine pcdmt3.13est} expression cassette to left-hand plasmid (p#30) and into E3 (in place of Cyda's E3 deletion).
- ii) Started cloning of CMV-14.7 expression cassette from pE1-14.7 (Terry-Chip) to left-hand plasmid.

2) Cancer therapy project

Have no plagues with SPB ↔ E4 promoter substitution. (293-TTF1 Mohan)

I'm starting with Rep/E4, ASH3/E4 from BT1, need to check them for ability to support growth of 366 (E4d1).

W162 - (expressing E4) - if Ann can find them. Growing up plasmids containing E4 under the control of CMV and native E4 promoters. (for cotransfection)

Valeri Krongliak wrote me that he would be able to send us 293/E4 (VK2-20) when Dr. Wold write him a letter with request. His address is on the next page.

TI-E4 deletion cassette.



Karoly 6/20/97

E3 proteins

- I am growing up ^{gp19K, pol II^{trans}} KT2 and ^{gp19K, pol II^{trans}} KT90 into the 15 cm dish
- I am doing a Western with KT4 and KT6
- I am doing a time-course with KT7 and C+ (KT10?)
- I am cloning R10 with CMV promoter into the shuttle vectors ^{Has in Kruppen's shuttle, Shaker shuttle.} R10 from Ad2 and Ad5.

Fork project

- I am ^{Have 2 plagues} growing the ^{clones} ~~clones~~ plaques. These plaques grow very slowly in 293/CrmA cells.
- M12 promoter is in pCI2Pac (Lynda) (maybe; probably)

Crm A

I have Crm A in Kruppen's shuttle plasmid, I am going to make virus with it.

Cancer Biology

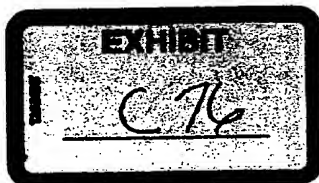
- I am fitting missing timepoints.

CMV-142 (Koty)
CMV-gp19K (Mohan)

We need maps and sequence of plasmids that they sent us.
Koty will check.
Especially the left hand plasmid with RSULTA/lacZ

Given to GTI 6/18/97
pCI-R10(5) } Chip
pCI-R10(2) }
pCI-gp19K

Will send to GTI next week.
pCI-14.7K (Loppreman)
Send to GTI next week



Valeri Krougliak,
Assistant Professor
Institute for Gene Therapy
Mount Sinai Medical Center, box 1496,
One Gustave L. Levy Place
New York, NY, 10029
Tel. 212-824-7748
Fax: 212-849-2437
E.mail krougv01@doc.mssm.edu

295 expressing EU (VK2-20)

Published in Human Gene Therapy 6: 1575-1586
(December 1995)

Have 3 plasmids with EU deletion.
Cannot rescue virus.



h/271 97 1451ya

1) E3 project

i) Cloning of CMV-E3 pm 734.1 expression cassette into left-hand plasmid and into plasmid with E3 deletion is in progress.

ii) Terry's pOI-14.7. Made miniprep of the plasmid, it looks like this is pCI with Ad5 14.7 in it. Made maxiprep, Karl is checking it for expression. Now doing recloning of CMV-14.7 expression cassette from this plasmid to left-hand plasmid.

2) Cancer therapy project

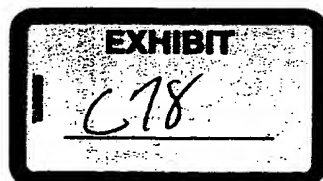
Got A549/E4; Hep/E4; W162 from Ann. Doing plaque assay of dl366 on these cells with 293 and A549 as controls.

Going to try to optimize transfection efficiency for these cells.

Going to try transfection-infection experiment (infection with 366, transfection with CMV-E4, SPB-E4 & E4-Epromoter as a control) on 293 cells.

Going to try cotransfect 293 with 1101/1107/E4R1 + CMV-E4 plasmid).

293/E4 (Valeri Krauszlik)?



PINE 3.95 MESSAGE TEXT

Folder: MAIL Message 41 of 42 90%

Date: Mon, 23 Jun 1997 17:28:35 -0600 (CST)
From: WOLDWS@SLU.EDU
To: "KROUGV01@DOC.MSSM.EDU"@SLU.EDU
Cc: WOLDWS@SLU.EDU
Subject: Request for cells

Dear Valeri,

I hope all is going well with you. I'm happy to see that you have a faculty position in a good university.

I am writing to request the 293 cell line expressing E4 (VK2-20) that you published in Human Gene Therapy (6:1575-1586, 1995). We have several plasmids with deletions in E4, and we have been unsuccessful in rescuing them into virus. We would use your cell line for that purpose.

Thank you in advance.

Sincerely,

? Help	M Main Menu	P PrevMsg	- PrevPage	D Delete	R Reply
O OTHER CMDS	V ViewAttch	N NextMsg	Spc NextPage	U Undelete	F Forward



970687

Gene Therapy Meeting

① Fast Ad

Karl

13 of Fast vector ~ 11 blue

(23 plaques total)

1 blue + killed MCF7 - control

3 plaques by PCR do have Fast gene.

PCR-Fast in Nipples left and shoulder. pBNG 11

Next

5 from 60 mm dishes

Check by IF - all plaques.

Check by PCR for Fast.

②

Ad-14.7 PGK vector - expression at 14.7 d pi

p734.1 - gp19 exp., 14.7K exp.

③

C⁺ kills cells at 2 days pi.

C50 stock - strange discrepancy between particles & titers.

Raffin → supernatant → perhaps some expression.

this plasmid expresses β-gal in transient/COs cells.

β-actin promoter & out enhancer; pol II for 14.7K.

This was done at 10⁸ PFU (titer could be much higher)

Repeat using titer calculated from OD & Dmazarov's gel.

This was better than β-actin promoter enhancer in COs.

Karl tried to make vector from several diff promoters/pGal;
this was only one that gave plaques.

GEL 1997:06:27 12:46:35, Range - 0.01-249.86 Counts, 1.00x

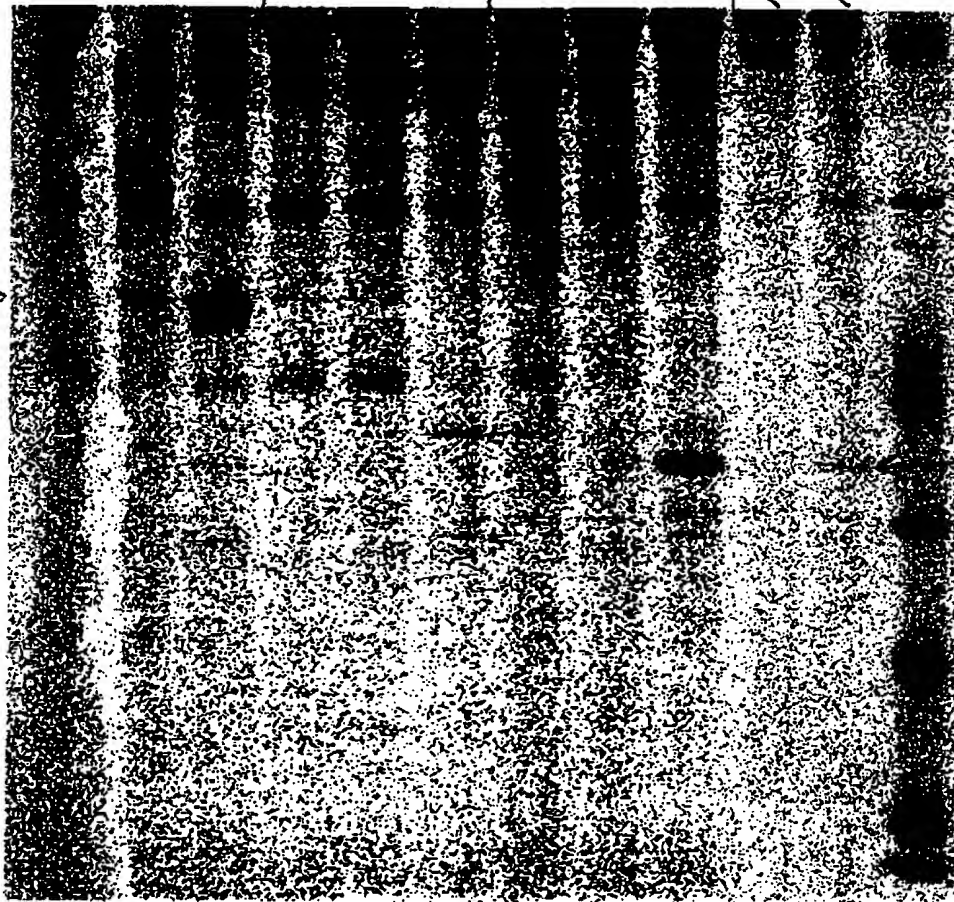
Karl

Transfection of p734.1 into 293

exposure
overnight on
PhosphorImager.

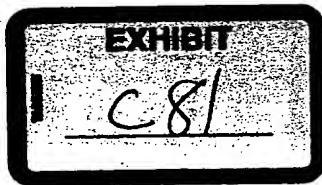
293	293 + 734.1	700 (200 pi)	293	734.1	700 (200 pi)	293	734.1	700 (200 pi)	AS219	AS219 + NFK-14.7B day 3 pi
-----	-------------	--------------	-----	-------	--------------	-----	-------	--------------	-------	-------------------------------

9p19K →



14.7K
in mod

α 9p19K	+	+	+							
α R1D/B				+	+	+				
α 14.7							+	+	+	+



Mohan, 6/27/97

1. C.F. project:

- a) 4 plaques (SPC Rep78 virus?) ^(uninfected CPE) are growing in 293 278 cells. 3 plaques showed CPE. Growth is slow ~ 60% confluent.
- b) RT-PCR for Rep78 antisense RNA were done. This week employing RNA + Reverse transcriptase to see if the PCR fragment is due to RNA and not from DNA contamination. It seems 293 (Rep78) cell line is expressing Rep78 antisense RNA.
- c) pSub VIII plasmid → chips → plasmid preparation. Elongation will make.

2. E3 project:

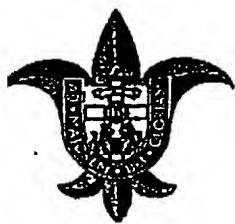
	Particles / OD	OD	ODU
d1704	2.4×10^{11}		0.77×10^{12}
d1722	1.35×10^{11}		0.77×10^{12}
d1731	1.44×10^{11}		1×10^{12}
d1739	7.7×10^{10}		1.72×10^{12}
d1753	1.07×10^{11}		1.18×10^{12}
d1762	1.58×10^{11}		3.18×10^{12}

d1704 ODU is lesser than pfu. (Repeat)
 - do 10^8 pfu + 10^9 pfu

EXHIBIT

C82

- b) MCF-7 cells transfected by p2E1SPN/gp12K and p*30 (Nimpen's) gp12K (*2, *3 & *7) got contaminated. (Yeast) Repeating again for I.F.
- c) Cloning Ad2, Ad5 RID into p2E1SPN and p*30 is in progress (from Karl)
- d) RTI (14.7 LacZ) gave 6.2×10^6 pfu → More CPE
 Stocks → 50000 - 100000



1402 South Grand Blvd.
St. Louis, MO 63104
Phone: 314-577-8432
FAX: 314-773-3403

**SAINT LOUIS
UNIVERSITY**

Department of Molecular
Microbiology & Immunology

Health Sciences Center
School of Medicine

Facsimile Transmittal

Date: 12-19-02

From: William Weld

Phone: 314-577-8432

Fax: 314-773-3403

Deliver to:

Dan Kaster

Phone:

Fax:

552-7305

Total number of pages including this page:

15

Message:

8 - 100MM

7/13

todo

phone:

Ab in white/red File on Arms desk

Inventory virus book * label / - Virus

✓ (KBS from freezer) / when brought up

3 day infection
use for
7001

Develop the gel (Monday)

$2 \times 10^5 / \text{ml}$

7.5×10^7

✓ (Cells frozen + thrown out) ✓

no less than 200%
3mls / 200mls cell

(1.5 ml / media)

Ad 1 + Ad 6 Virus stock (5mls of stock)

Set up
1-100ml → stock

grow up

11.6 pre-Absorbed. ✓

Set up *

293 cells from Kaye (Duke Univ) OK

Ginsberg-H501 III (earliest stock) (175 flasks)

V9103 5-2-1 stock 50ml → 100mm plate → flasks

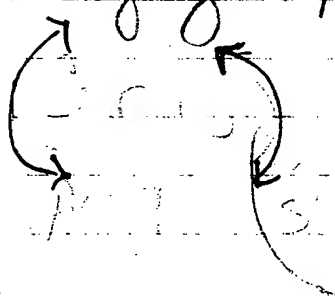
V9103 5-4-1 spin down media 20% FBS 100ml → 100mm plate

(harvested) (960705)

Bayley 11/07/6 (911003) 104-8 1x

50ml → 100mm plate

freeze thaw
harvested (960725) 104-8



9/4/96

CSC Banded the virus Ad1 960825
1101/1107 Baileys (960802)

- 1 freeze (thaw)
- 2 sonicate X 2
- 3 Vol after son 1101 < 21mls

Ad1 < 19mls

add $V \times 0.51 = g$ of GCL

10.71g in 1101/1107 Baileys
9.69g in Ad1.

infect 3 liter spinner with
dl 717 Vp 891208 Titer 1.3×10^{11}

cell count 3 liter 3.5×10^5
Vol = 3 liters (3000mls)

$3.5 \times 10^5 \times 3000\text{mls} = 10.5 \times 10^8$ total cells

use 20 pfu's / cell

$\frac{1.0105 \times 10^{11}}{1.3 \times 10^{11}} \times 20 \text{ pfu's}$
162ul : use

KB's are healthy no clumping.

EXHIBIT
D2

9/17

~~9/18~~

1. Atlanta 6013E
 $\frac{19}{4} \times 3 =$

first
 1.4 (cells are shriveled up)
 $\times 10^5$

* 2. Bawhitakee
 6m1228
 $\frac{28}{4} \times 3 =$

cells look very healthy
 2.1×10^5

3. NYC Apa 4819
 $\frac{31}{4} \times 3 =$

Nice + healthy cells very
 flat + round
 2.3×10^5

4. present 4m1938
 $\frac{21}{4} \times 3$

Cells are dividing now
 smaller cells but healthy
 1.5×10^5

5. NYC AF B4870
 $\frac{22}{4} \times 3$

cells look great
 1.6×10^5

6. B10W 6m0741
 $2\frac{1}{4} \times 3$

strange shape of cells
 Rough edges not round
 1.5×10^5

infected 3 liter spinner with
 1101 / 1102 20 mls
 3.2×10^5 cells/ml

EXHIBIT
 D3

September 18, 1996.

Cloning EcoRI-Xba B fragment to pBSSK(+)/EcoRI+XbaI
of pFG140

Lanes: miniprep of:

1) pBSSK(+)

2) - 9) clones

10) - 12) p21 (Mippen's) plasmid

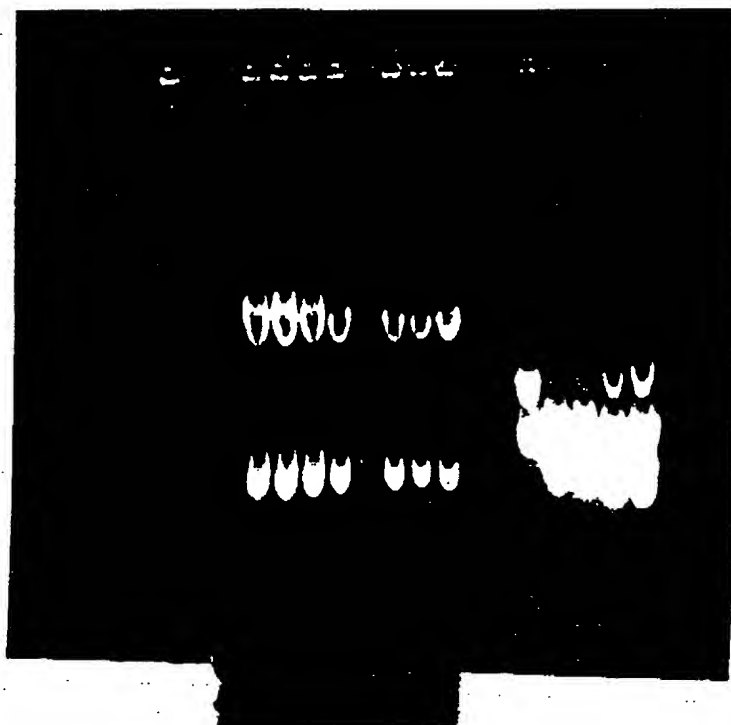
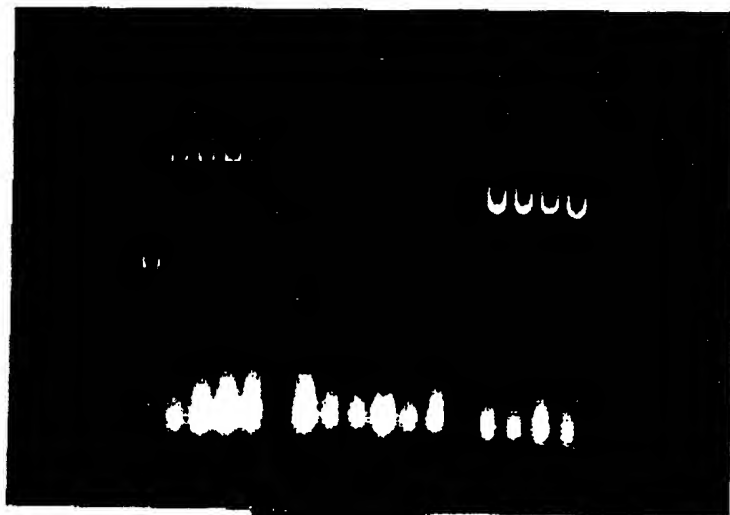
14) - 17) pISP-E3.7.

First experiment
09/18/96

Restriction patterns of
the plasmids.

- 1) Ladder
- 2) vector (pBSSK(+)) RI/XbaI
- 3) fragment B pFG140/RI/XbaI
- 4) - 11) - RI+XbaI clones 1-8
- 13), 14) - p21 (Mippen) EcoRI
- 15) - 18) - pISP-E3.7 Nde + EcoRI

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



EXHIBIT

D4

pBSKS(+) + 8 hr. nt pFG/wo RI/10g

(pK1)

Lanes : 1) Ladder

2) RI + Nde I

3) Bst 1107 I

4) Sun I

5) Bst 1107 I + Sun I

mild
core

⇒ size of RI-Nde fragment?

⇒ RNA masked 600 bp ~~RI-Nde~~

Bst 1107 I - Sun I fragment

2% agarose gel

1) Ladder

2) pK1 / Sun I + Bst 1107 I
+ RNase

⇒ 600 bp fragment

EXHIBIT

DS

Checking the restriction
pattern of plasmas

in ladder

2) L1 / NHe + R1

3) L1 / X49

4) L2 / NHe + R1

5) L2 / R1

6) L3 / NHe + R1

7) L3 / R1

EXHIBIT

DC

28 September 1996.

minipreps.

1) Ladder incl.
 2, 3, 4) - pLSP-B 2.2
 5, 6, 7) - L2 \Rightarrow
 \Rightarrow pLKHE2A + Bam \rightarrow end + cle

8, 9, 10) - L3 \Rightarrow
 \Rightarrow PCR(LKH dP) Bam \rightarrow end E2A+

SPB experiment
 10/27/96

minipreps.

1) Ladder
 2) - 8) - L1 \Rightarrow
 \Rightarrow pTZAd-Xba.

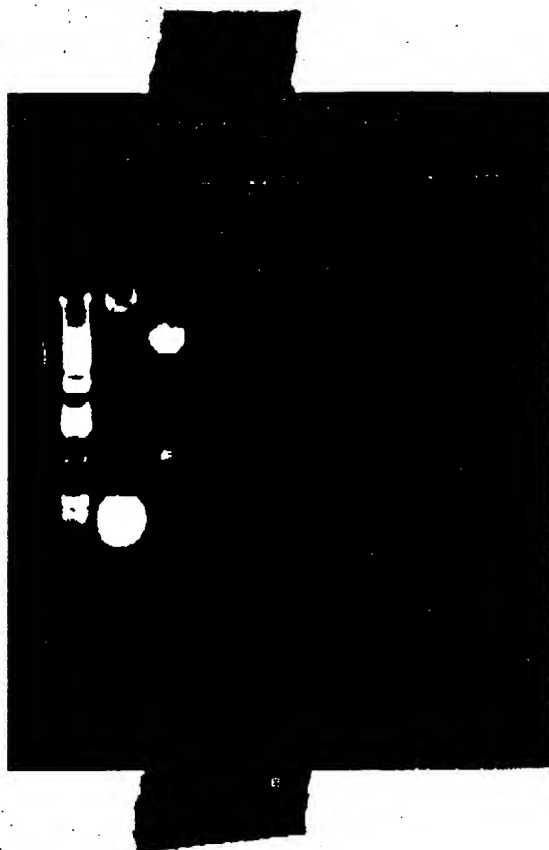
EXHIBIT

D7

September 30, 86.

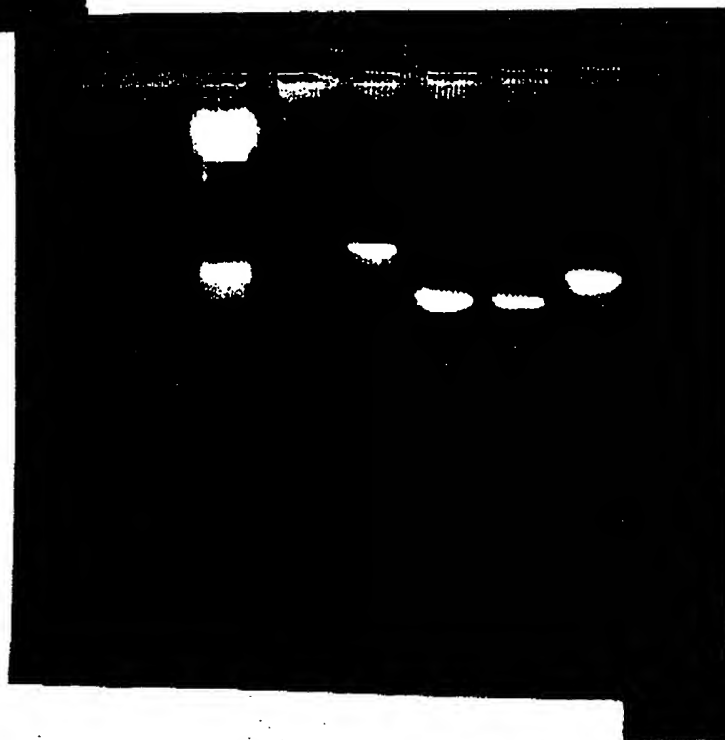
Cloning of Cuv promoter into
Bst 1107I site of p21 (Nipha).

- 1) ladder
- 2) p21 / Bst 1107I
- 3) pCDNA3 / Bgl II + Bam HI



October 2, 86

Testing primers in PCR



- 1) Ladder
- 2) KJ2 - KJ3
- 3) KJ1 - KJ2
- 4) KJ4 - KJ5
- 5) KJ6 - KJ7
- 6) KJ8 - KJ9

→ all 9 primers
are OK.

22-143 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



October 9, 96

Analysis of clones

1-2, 4-8

pK1 / Bst1102I + SclI + CIP
+ 19K* (with mutation)

1) ladder

2) pK1 / RI + PacI

3) - 9) - clones / RI + PacI

clones 1, 4 - 8 \Rightarrow recombinant \Rightarrow clone 2 - wt. \Rightarrow name recombinant
plasmid (PK2)

October 21, 96

Analysis of miniprep
restriction

1) pL2 / SclI

2) - 8) clones

1-7 / SclI

3) - ladder.

 \Rightarrow 1, 4, 7 - recombinant
orientation?Cloning KDI ADP
10/11/96

EXHIBIT

D9

October 27, 96.

Analysis of miniprep
by restriction.

- 1) Ladder.
- 2) p21 / KpnI.

- 3.) - (14) clones

p21 / Bst + CMV prom.
Bgl + Bam + Klenow →

→ clones 125 - 131. Kpn

clones 25, 26, 28, 31
the orientation that I need
(allowing transcription)clones 27, 28, 29, 30, 31, 32
35, 36 → other orient.+ clone 23 from
after cloning is ok.15 - 26) clones p21 / Bst + PCR product -
- promoter SP-B (500 bp) with Bst I sites
on the ends

⇒ clones 225 - 231. / KpnI

⇒ clones 27, 28 ⇒ correct orientation
+ clone 23 from previous cloning

clones 25, 31, 32 ⇒ other orientation.

Cloned SPB prom.
in E4 10/26/96

EXHIBIT

D10

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

$C_{primer} \approx 70 \text{ pmoles}/\mu\text{l}$

361/1380 SmB / \Rightarrow to sequence 3ex (1912*)
 1741 KpI use W1 and C13
 140/1981 BstI

Wednesday, October 30, 96

- 1) 3ex clone 1, 4(?) - need preparation for sequencing
- ✓ 2) Purify ADP-Xba fragment, purify pL1/Xba/CIP vector

Ligation: insert (ADP-Xba) 0.15 $\mu\text{g}/\mu\text{l}$ vector L1/Xba/CIP 0.10 $\mu\text{g}/\mu\text{l}$

control 15 μl v.o. 5 μl vector

4 experiment 15 μl insert 5 μl vector

+ 5 μl buffer (5X) + 1 μl ligase \rightarrow 1 hr room temp.

Thursday, October 31, 96

- 1) 203 cells tomorrow will be ready to pass \Rightarrow prepare HEBS and ~~cells~~ What about 2x media?
- 2) Sequence 1!
- 3) Prepare new ADP-Xba insert / Ligate, transform
- 4) Order primers for sequencing p2 inserts
- 5) first, repeat PCR with p2a
- 6) Mahan about TP-2 and ADP

$$C = 7.88/\mu\text{l} = 0.0788/\mu\text{l}$$

Cloning K03 ADP

EXHIBIT

D11

Sequencing

pC2 (8p14k*) \Rightarrow clone 1

- Mix - 8 μ l
- Template - 1 μ l
- Primer - 5 μ l
(KD1 or KD3)
- H_2O - 8 μ l

P.T. Temp 96°C

96°C - 30"

50°C - 15"

60°C - (4 min!)

25 cycles \Rightarrow KD1 ~~2~~ KD3

HEBS 2x for 200 ml

- ▼ 2 g HEPES
- ▼ 3.2 g NaCl
- ▼ 0.148 g KCl
- ▼ 0.039 g Na_2HPO_4 (anhydrous)
- 0.4 g glucose

final pH = 7.0.

 $CaCl_2$ 2.5M

MW = 147.00

for 100 ml

36.75 g ▼

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

EXHIBIT

D12

Friday 1, November, 1986

- 1) Prepare HEBBS, CaCl_2 , test recipient, filter
- 2) Run $\frac{1}{2}$ of 3 pfu, ^{cut with Xba} ^{run c. 1000 bp} fragment, ^{transformation} ^{disk}
- 3) Cut TP-DNA with EcoRI , ^{check on gel}
- no fragment? repeat, take pF640 as template!!!
take other pfu polymerase!!!

Saturday 2, November, 1986

- 1) Set up cells on 6 cm dishes @ dishes.
- 2) Prepare HEP (0.1 M), NaOH (0.1 N) for cell culture.
- 3) Cut TP-DNA with EcoRI , run electrophoresis.
- 4) PCR AD-Xba with pfu, pF640 as template.
- 5) Filter sterilize Carlsberg carrier DNA (salmon sperm DNA).

PCR with pfu

100 μl template (1 \rightarrow 1000 pF640) ●
 2 μl primer (4) ●
 2 μl primer (5) ●
 180 μl H₂O ●
 20 μl buffer for pfu. ●
 2 μl pfu ●
 4 μl dNTP. ●
 200 μl ●

Sunday 3, November, 1986.

no PCR product, buffer pfu?

- 1) Cut Pqg PCR product AD-Xba, with XbaI .
- 2) Transfection (pF6 100. — 20 μl (100))
 each TP-DNA spl + carrier — 10 μl (100)
 on 2 dishes (TP-DNA spl + pF2 20 μl (200 pF2X60)

EXHIBIT

D13

Monday, 4, November 1996. (clavary note volume!)

- ✓ 1) Purify fragment ADP-obs, ligate, transform DH5α.
- ✓ 2) When transforming DH5α, seed cells on SOB-agar for preparing competent cells.
- ✓ 3) Order primers for sequencing plasmid.

Ligation $\frac{\mu\text{g}}{\mu\text{l}}$ vect (L1) = 0.1/1
 $\frac{\mu\text{g}}{\mu\text{l}}$ insert (ADP-obs) = 0.01/5.

Ligation (promega)

control 1.5 μl vect + 5 μl H₂O + 1 μl ligase
 exp. 1.5 μl vect + 5 μl fragment + 1 μl ligase \rightarrow 2h room temp.

! Sequencing failed \Rightarrow too low p_{xy}!!!
 Repeat with both primers 3x more template
 3x more primers

mix \rightarrow 8 μl
 template \rightarrow 4 μl
 primers

1/3 = dilute 1/10
 take ① - 2 μl (3)
 ② - 2 μl (5)

+ 6 μl H₂O (1)
 + 4 μl H₂O (3)

! There are no E3 poly A_{ta} sites in L2!
 May be it can use fiber's gene p_t?
 Moreover, there are no acceptor splicing site
 in your construct, how can it be expressed?

Check literature on expression of inserts in the
 deletion of E3.

Splicing in Ad, esp. E3 splicing.



22-141 50 SHEETS
 22-142 100 SHEETS
 22-144 200 SHEETS

EXHIBIT

D14

Tuesday 5 November 1996.

- 1) Repeat sequencing : 3ex 1 clone. primers 1 and 2.
- 2) Seed clones new 4ex (5 clones) on sectors.
- 3) Prepare competent cells DH5 α .
- 4) Check ~~clon~~ ^{clon} number insert into p21 with other restriction sites, start clone it into p21.

Sequencing \rightarrow with primer 3 have a precipitate.
with primer 1 precipitate is much less.

Wednesday 6, November 1996

- 1) Extract plasmids from clones 4ex (5 clones), check if they are restriction sites.
- 2) 4) - from yesterday.

Thursday 7, November 1996.

- 1) Seed clones too liquid culture for miniprep with Wizard Plus miniprep kit for sequencing.
- 2) PCR with pFur of ~~ADP~~ ^{ADP} (primers 4, 5)

75 μ l - H₂O
1 μ l - template p21 (no.)
10 μ l - ~~buf~~ ^{buf} pFur
1 μ l - primer 1
1 μ l - primer 2
2 μ l - dNTP
1 μ l - pFur
10 μ l - DMSO

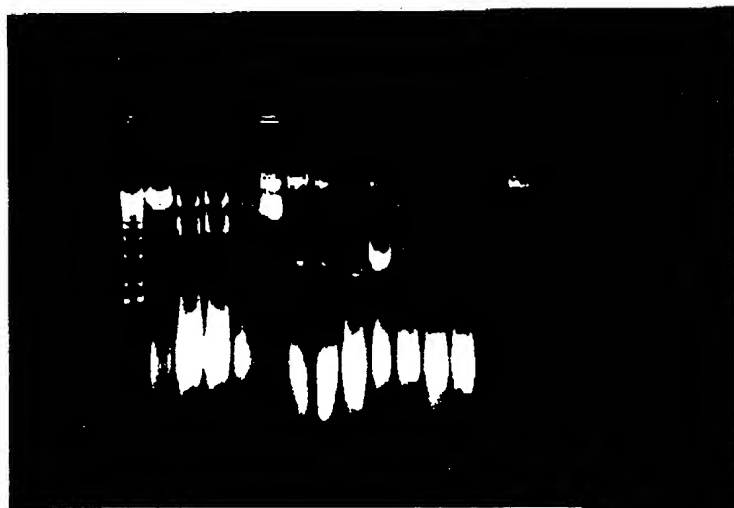
- 3) Prepare vectors Lit/Xba and pB1611 / ~~Scor~~ ^{Scor} I \rightarrow large fragment.
- 4) Check ~~clon~~ ^{clon} in p21 (Nde I)
- 5) Check ~~clon~~ ^{clon} wanted DNA for mut?
- 6) PCR of inserts into p21, with SP-B it is possible to check orientation!

EXHIBIT

D15

hru 11, severe xel electrophoresis.

- 1) - Ladder
- 2) - 21
- 3) - 123 Juncos (Butler D, orange).
- 4) - 128
- 5) - L1
- 6) - 10) 1-5 clones rep.
- 11) - 14) L1/Xls prep.
- 15) - pBHG11 / RI prep.



Conclusions!

1) it's on with em
ponder (L1)

2) it's on with
pBHG11 RI

3) L1 clones → trash
4) L1/Xls → trash

November 10, 1996, Sunday, November 11, 1996, Monday

- ✓ 1) Split 293 cells on new flask.
- ✓ 2) Overlay 293 dishes with neutral red.
- ✓ 3) Run electrophoresis of Wizard minipreps and L1/Xls.
- ✓ 4) PCR of clones + electrophoresis.
- ✓ 5) ~~PCR~~ CIP pBHG11/RI, cut from the gel?
- ✓ 6) Get p21/GMV with EcoRI, get the fragment from the gel?
- ✓ 7) Change the medium in 293 flask.
- ✓ 8) ~~New prep. of L1?~~ Clean up old preps?
- ✓ 9) Seed 54, 57 and L1 for Wizard miniprep!



22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

EXHIBIT

D16

Tuesday 12, 1996

Cannot cut 2PM after w. seed kit in prep.

- 1) 123 - with EcoRI - faint, take from gel
 2) L1 - with XbaI - large fragment!

Wednesday 13, 1996.

- 1) CIP purify, cut fragment from gel, cut fragment 123/R1
 2) Try to cut L1 with XbaI, if not successful → seed L1

- 3) Ligate from 1)

12 pl vec + 5 pl insert + 1 pl enzyme
 + 1 pl H₂O - control

L1/XbaI - not in single band. Extract with w. seed → seed it in ligase culture

pBAG11/R1/CIP - A - fragment - not single band →
 ready to distinguish between all this forms.

Thursday 14, 1996.

- 1) Transform DH5α with ligase mix from yesterday
 (Try to obtain high efficiency!!!)

- 2) Extract 4L with Wizard, cut XbaI, run together with yesterday's L1/XbaI (control) on 1% gel.

- Try PCR! Maybe you can use it for screening 9/12!

- Sequencing with new batches of 3.1!!!

PCR (Taq polymerase)

for 150 pl

- 15 pl buffer
 3 pl dH₂O
 4.5 pl MgCl₂
 1 Taq pol
 130 pl H₂O

- 1) 123 } primers 10, 11
 2) 125 }
 3) 223 } primers 8, 10
 4) 227 } primers 9, 11
 5) p21 - control (-) } check presentation

19 54 } primers 6, 7

11 52 }
 12) pL2 - control (-)

19 reactions

15 (10-11)
 2- (9-10)
 2- (8-9)

13, 14, 15 } cut 54, 57 with PstI
 L1 - control

125 with Bst 11044
 127 - control

EXHIBIT

D17



**SAINT LOUIS
UNIVERSITY**

1402 South Grand Blvd.

St. Louis, MO 63104

Phone: 314-577-8432

FAX: 314-773-3403

Department of Molecular
Microbiology & Immunology

Health Sciences Center
School of Medicine

Facsimile Transmittal

Date: 12-19-02

From: William Wald

Phone: 314-577-8432

Fax: 314-773-3403

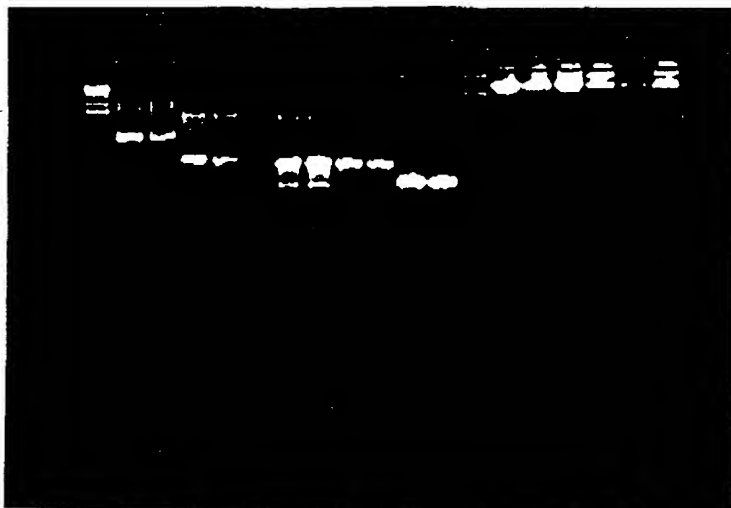
Deliver to: Dan Kasten

Phone: _____ **Fax:** 552-7305

Total number of pages including this page: 15

Message:

See explanation
of the picture
on
previous
page.



Conclusions: everything is fine
except that Anti1/b2I didn't cut DNA
(because of buffer 4, I think).

Friday 15, 1996.

- 1) ~~Transform L1~~! Clean up L1 preps., try to cut with Xba
- 2) Seed clones of pRH611 + 123 (cut).



22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

EXHIBIT

D18

HALE 294 W138

Friday (1:00 /

Monday, 18, 1996

✓ 1) Analyse clones (1-24) pBUG11/A1 + CMV (128 clones)
run on gel and then cut with Nde I

✓ 2) Phone about Srf I.

✓ 3) Transform L1.

✓ 4) Sequence PCR

✓ 5) Prepare TP-DNA, TP-DNA/R1, Ad5 DNA, Ad5 DNA/R

✓ 6) Split 293 to dishes for transfection

Sequencing.

✓ 8 µl pre mix

✓ 5 µl p31 (0.58)

✓ 1 µl primer (v1) 1)

✓ 6 µl H₂O

✓ 20 µl oil

circling.

✗ pBUG11 gave 2 small fragments instead of 1.
~~check~~ what is it?

clones gave incomplete digestion → O/N NdeI
after PEG precipitation

Thursday, November 19, 1996.

1, 3, 5, 6) from yesterday.

if fail in 1), do PCR with 10, 11 primers!

Freezer at CR room 3 shelf from top

left drawer

upper box (-9)

tube with 918 on cap

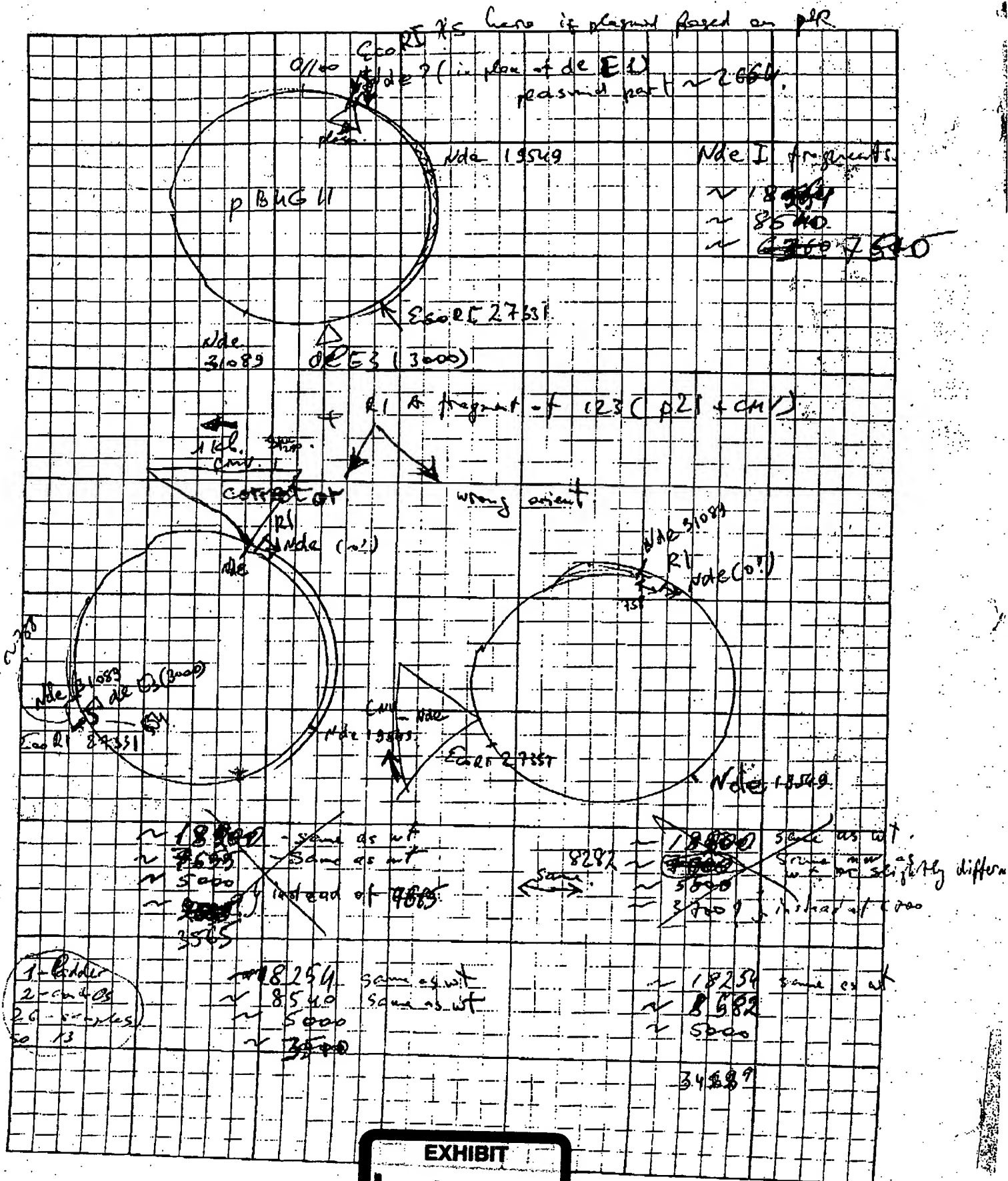
(VS 20.) on side

→ Ad5
CSA

EXHIBIT

D19

or it's here if played based on pR

**EXHIBIT**

D20

← But it is not like this with ~~EcRI and NdeI~~
 because you were able to see
 & it's like this, leave NdeI digestion of p21
 gave linear form.

⇒ Incomplete digestion? (with Nde)

⇒ cut with Eco RI
 and Pac I + Bam HI (pBHG II as control).

1) ladder
 minipreps: 2) pBHG II / Nde
 (6 ex)

3-26) - clones 1-24

⇒ clones 4, 7, 9, 14, 18, 21
 → trash.

clones 1, 2 and other
 with same pattern are
 with correct orientation of
 insert?!

Partial digestion with
 NdeI!

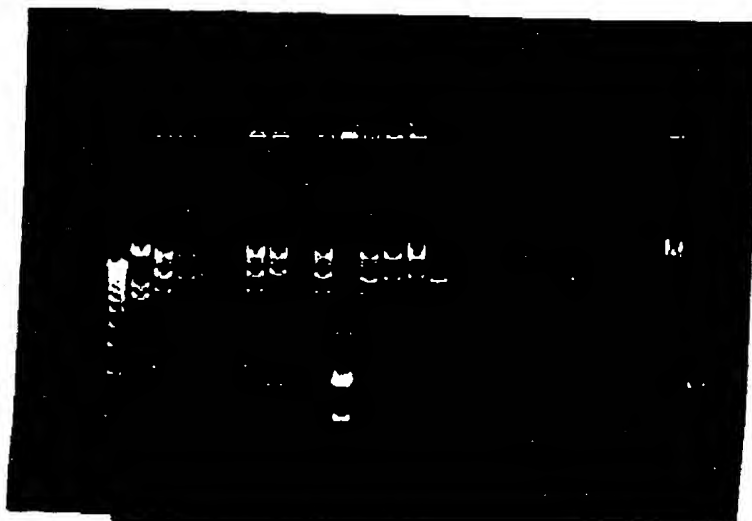
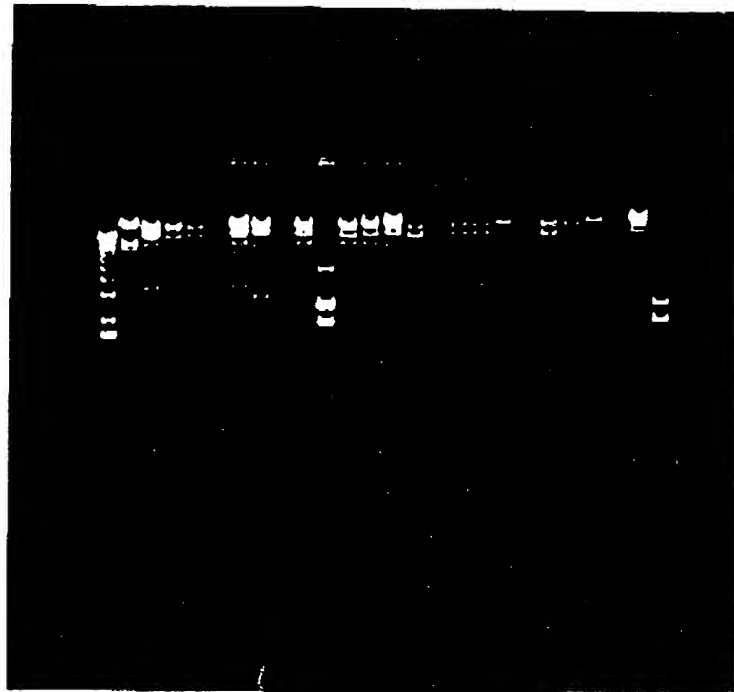
Bottom picture is the
 same.

or cloning is partially
 digested pBHG II
 or star activity digested?

take to analyze RI

1, 3, 5, 6, 17, 19, 21

22-141 50 SHEETS
 22-142 100 SHEETS
 22-144 200 SHEETS



EXHIBIT

D21

Pac + Bam → NEB Buffer (4) = green.

both enzymes

~~NEB Buffer (4) = green~~
EcoRI → (multi core) → Buffer 4, Promer.



1) Badder

2) B611 / R1

3) 1

4) 3

5) 5

6) 8

7) 12

8) 13

9) 21

(10) B46 / Bam + Pac

(11) 1

(12) 3

(13) 5

(14) 6

(15) 17

(16) 14

(17) 21

(18) 18

Conclusions! 17, 21 are OK by EcoRI digestion
others are result of EcoRI star activity
when preparing vector.

Pac + Bam → pBUC11 gave more fragments than
expected.
all clones are similar and different
from pBUC11. Wrong orientation?
They have different orientation.
Pac did not work in clones?

17, 21 are not OK inserts are too small. 11/27/99

EXHIBIT

D22

2 orientations

10000

11000

8000

7500

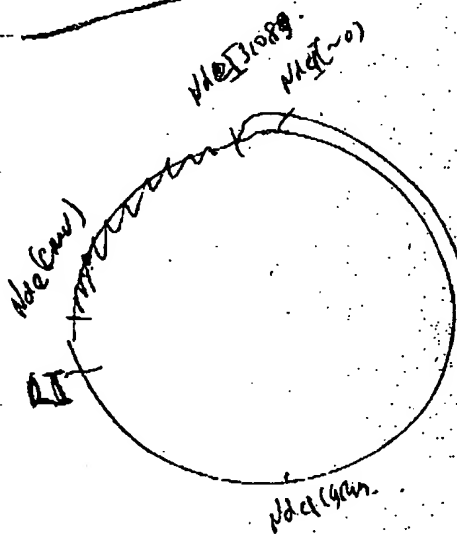
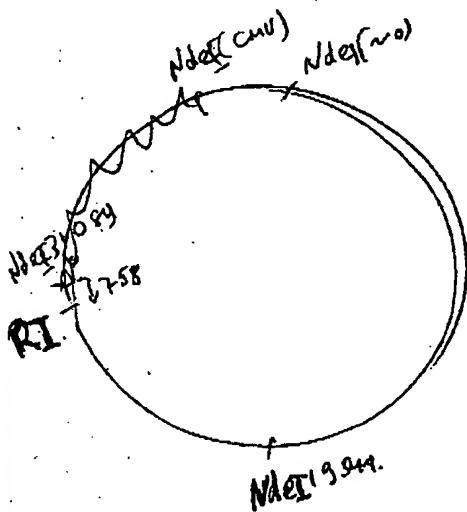
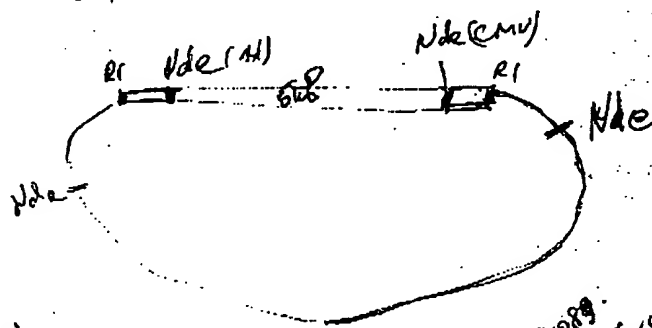
5000

5000

3000

2700

you can explain
it just in the case
if larger fragments of
are part of a
partial hydrocarbon



22-141 50 SHEETS
22-142 100 SHEETS
22-143 200 SHEETS

EXHIBIT
D23

if it is mixture of 2 plesmids
and \Rightarrow there are just 2 pdc sites?

EXHIBIT

D24

Wednesday, November 20, 1996.

Thursday 21 November

- 1) Seed L1 for mini (midi) prep. with Wizard!
- 2) Cut TP-DNA Ad5 with Eco RI, check on G/E, did lize against TE.
- 3) Precipitate Ad5 DNA, check amount, cut Eco RI, phenol, precipitate.
- 4) Split 293 to dishes for transfection.
- 5) Sequence clones.
- 6) Prepare new vector pBHG/RI/XIP, ligate with 123/RS insert.
- 7) Seed 17,21 clones for further characterization. extract with Wizard kit!
- 8) Cut pBHG with RI, Nde, (Bam, Pst), (Bam + Pst) (at the Pst).
- 9) Check SbfI site in pEG140, pBHG, p1, some other?

Friday 22, November 22, 1996.

- 1) Transfection of 293 with pL2 + TP-DNA Ad5/RI or ~~AD5/RI~~
- 2) Extract 17,21 and L1 with Wizard miniprep.
- 3) Sequence clones.

seq #2 3 ex, clone 1 (31) - primers 10, 11.

seq #3,4 2 ex, clone 23 (223) - primers 10, 11

seq #5,6 1 ex, clone 23 (123) - primers 10, 11

seq #7,8 5 ex, clone 4 (54) - primers 6, 7.

8 µl promix
 5 µl template (0.58)
 1 µl primer
 6 µl H₂O

40 µl oil
 circling

EXHIBIT

D25



Monday, November 25, 1996.

- 1) Cut new preparation of L1 with Xba, check on G/A.
- 2) CIP (BAGH/R1).
- 3) Check amount of H5/R1.
- 4) Cut 17,211 with Bam + Srf, p64611 - control. → mt. fragment 5858
- 5) Check plasmids with Srf I.

Spa I - site → 250 in chrV promoter.

⇒ in right orientation → fragment ~ 5800 bp

⇒ in wrong orientation fragment ~ 1000 bp.

wt - linear form.

BAGH/R1
H5/R1
L1/Xba
BAGH/R1
H5/R1

1) ladder

2) p64611 + Bam +

3) p64611 + Srf I

4) p64611

5) L1 - D

6) L1/Xba - C

7) L1 - M

8) BAGH/R1 (in buffer H)

9) H5/R1 (in buffer H)

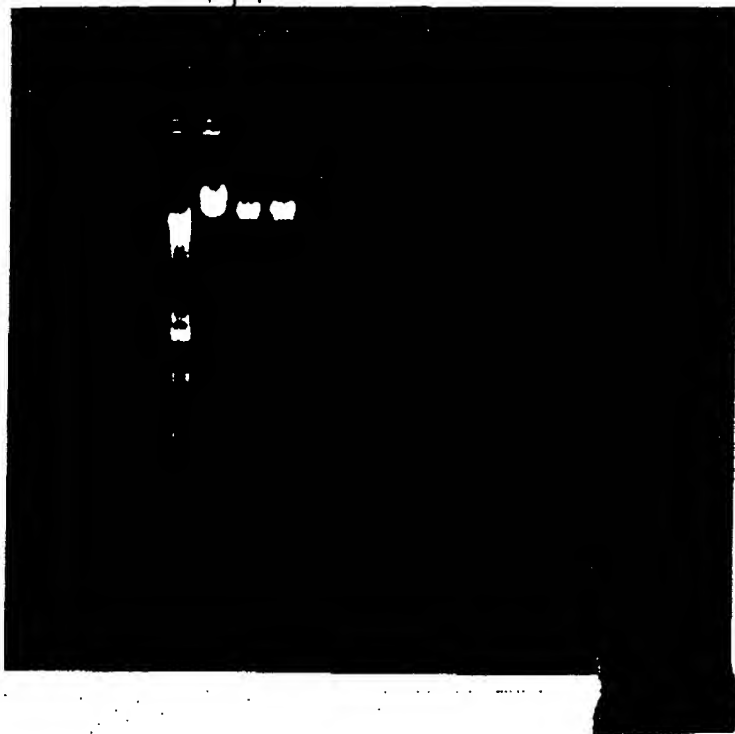
Arrows
buffers

Bam + Srf hydrolysis (in buffer H) - strange
picture, same as before Bam + Pac → m.b.
2 Bam sites or star activity?

EXHIBIT

D26

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



- 1) ladder
- 2) 046119
- 3) done 17 Spe I
- 4) done 21

there are no fragments
~ 6000 bp →
→ wrong orientation
or what?
→ repeat cloning.

EXHIBIT

D27

Tuesday, November 27, 1996

1) pGEM1/EI/CIP → extract from gel
 L1/Xba → CIP → extract from gel
 ligate to inserts o/n 3(PCR)/Xba → extract from gel (2%)

2) PBK6 (1/EI/CIP (new prep, 0.1/1) → 12 μl
 1.2.3 insert (old prep, 0.05/1.5) → 7 μl

2 μl buffer
 1 μl enzyme

o/n 16°C

1) PL1/Xba/CIP (new prep, 0.1/1.5) → 12 μl
 3(PCR)/Xba insert (new prep 0.1/1.5) → 5 μl
 → 2 μl buffer
 → 1 μl enzyme.

o/n 16°C

Wednesday, 28, 1996.

1) Transform DH5α cells with ligation mixtures from yesterday, try to obtain high efficiency!
 plate cells in duplicates, 1/10, and all.

2) Plan scheme of experiments to obtain larger plasmids, check everything, start cloning.

3) Split 293 in flask.

Friday 30, 1996.

1) Seed clones 6ex, 4ex in liquid culture and agar plates.

2) Split 293 cells, overlay 293 dishes with transfection.

EXHIBIT

D28

Saturday, November 30, 1996.

1) Extract 6ex 25-36 with Wizard kit, cont. with
 SpeI. Extract uex 1-24 with
 ant with Sac II.

2) from yesterday.

SpeI - NEB Buffer II.

Sac II - buffer C / orange

3) Check references about splicing in Ad, especially
 in ES and fiber!

4) Start with genes IL and IV?

* Filter NEBS and cell₂ from freezer 2 time?!

WB

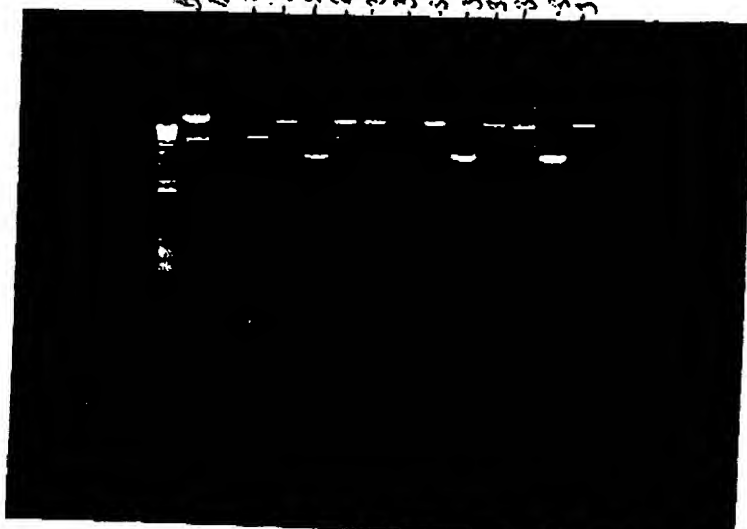
There is no SpeI site in CMV promoter according
 to my sequence \Rightarrow may be clones 17 and 21
 from previous cloning are OK?

Sunday, December 2, 1996.

1) Check new 6ex clones with EcoRI, select recombinants

2) Check new 4ex clones with XbaI, select recombinants

Bug 11/RI
 125/RI/146
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36



1)

1) ladder

2) 04611/RI

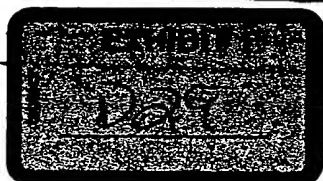
3) 125/RI \Rightarrow A fr.

4) \Rightarrow 25-36

Recombinants

26, 28, 29, 31, 33, 36.

2) Can't see
 fragment
 on XbaI hydrolysis.



3) Hex ScaI (1 site in ADP), no sites in L1.
 + RI (0 sites in ADP), 1 site in L1.
 expected fragments correct orientation ~1261
 wrong orientation ~1561
 orange buffer (C)

4) 6ex clones Pac + Bam .

1h Pac (buffer NEB1 + BSA)

↓ heat inactivate

↓ + 1x buffer (E)? + Bam → 1h → E/E.
 (E)?
 (D)?

NEB 1 - 10 mM Tris propylene-HCl, 10 mM MgCl_2 , 1 mM DTT (pH 7.0)

BamHI - 150 mM NaCl, 10 mM Tris HCl, 10 mM MgCl_2 , 1 mM DTT (pH 7.9)
 unique NEB
 buffer.

buffer D - pH 7.9, Tris HCl - 64M, MgCl_2 - 6 mM, NaCl - 150 mM.
 orange
 D - yellow.

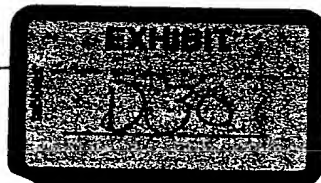
buffer C (orange) pH 7.9, 10 mM Tris HCl, 10 mM MgCl_2 , 50 mM NaCl

buffer (white) pH 7.8, Tris HCl - 25 mM
 acetate

100 mM K acetate, 10 mM Mg acetate.

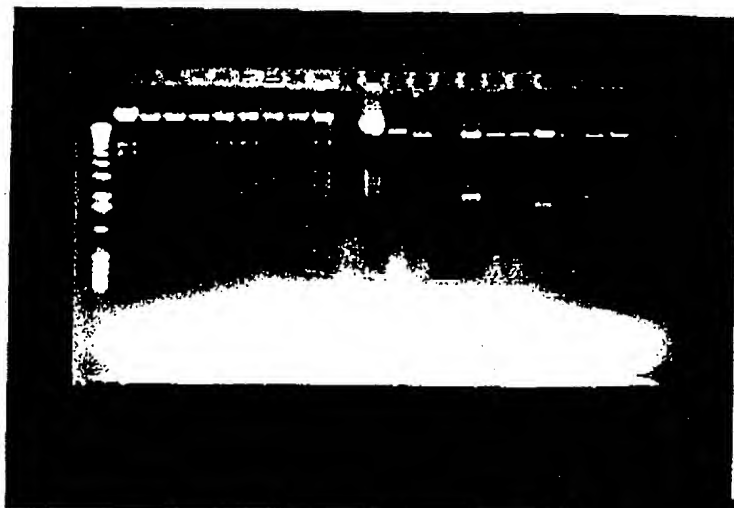
Take orange 2X?

22-141 50 SHEETS
 22-142 100 SHEETS
 22-144 200 SHEETS



Cloned 603 AOP

12/2/96



1) ladder

2) pM11 / Pac + Bam

3) 17

4) 21

5) 26

6) 28

7) 29

8) 31

9) 33

10) 36

11) blank

12) L1 / Sac II + R1

13) - 241 - clones

hex (1-12) / Sac II + R

the same gel,
higher magnitude.

Conclusions:

hex -

- clones

2, 5, 6, 7, 8, 10 -

- correct orientation

clones 4, 9, 12 -

- wrong orientation

hex - absolutely

unclear
what is happening.

yellow ←

Tomorrow try to cut with Nde I,
take 10 μ l of plasmid, good activity
of Nde I.

Try some other enzymes? (Not Pac
Not Bam)

universal
IX.

for example Spe I, Srf I.
correct or → 448

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS





**SAINT LOUIS
UNIVERSITY**

1402 South Grand Blvd.

St. Louis, MO 63104

Phone: 314-577-8432

FAX: 314-773-3403

Department of Molecular
Microbiology & Immunology

Health Sciences Center
School of Medicine

Facsimile Transmittal

Date: 12-19-02

From: William Wald

Phone: 314-577-8432

Fax: 314-773-3403

Deliver to: Dan Kaster

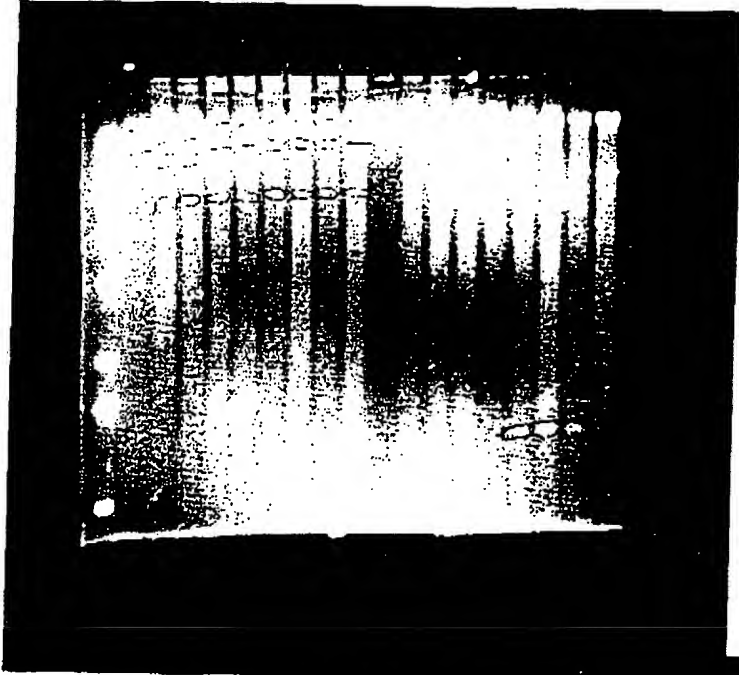
Phone: _____ **Fax:** 552-7305

Total number of pages including this page: 18

Message:

Tuesday, November 5, 1996

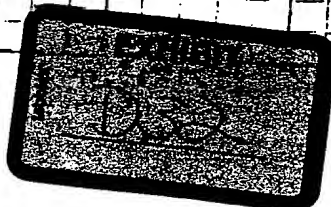
- 1) cut 600 clines with Ndc (Ref. I), yellow
and Grf + Spe I (Kitt universal 1X)



Conclusions: 17, 21, 29, 37, 33 - one orientation
26, 28, 36 - other orientation

If consider the previous picture, 26, 28, 36 → correct some further,
because there was additional 64p Rn-Bain
fragment.

Obviously, there is Spe I site in CNV
didn't give fragments because they are
wrong orientation of an Spe I hydrolysis



Wednesday, 4, 1996

1) Cut cex clones with SpeI. (buffer Multicore)

1) ladder

2) pB4511 / ~~SpeI~~ SpeI

3 - 100

17, 21, 26, 28, 29, 31, 33, 36
- SpeI

there is fragment

6 kb in (26, 28, 36)

⇒ correct orientation

there is fragment

1200 bp in 29, 31, 33

⇒ wrong orientation

17, 21 - junk! Look
also to upper fragment
on the previous picture.

Conclusion: When everything is OK, it's OK.

Friday, December 6, 1996.

1) Cut pFG140 → BamHI + NdeI fragment (9437)
(contains EcoRI site, other fragments do not).
other fragments ~ 2500 - if there is no NdeI in pFG?
at 1200
Go on
if there is NdeI.
2043

at 223 (p110508) with NdeI + BamHI - vector

2) Split 293 cells.

3) ~~Reseed~~ Reseed clones to new dish.

4) ~~Grow~~ Grow

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



EXHIBIT

D-5

Monday, December 3, 1996.

- 1) 1) and 3) 4) from Friday.
- 2) Prepare LR for preparation ~~gating~~ of Gex.
Inoculate LB overnight (15h).
- 3) Prepare the HRP pH (8.5) (8.0) (7.5) (7.2),
autoclave.

Can use 1104/1107 for ~~contamination~~ to attempt
to obtain a virus with E4 promoter \rightarrow SP-B promoter
substitution.

- 4) Start cloning EcoRI-SalI fragment pFG140
into pK2 (gp19K+)

Bank I - Nde - Buffer)
pFG140 Sal - EcoRI - Buffer)

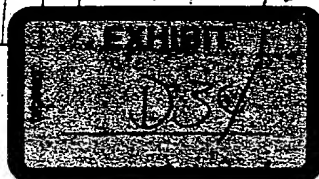
223 (p21 + SP-B promoter) - Nde - Bam HI - Buffer) - vector
pK2 (31, gp19K+) - EcoRI - Sal I - Buffer) - vector.

pFG140 Sal - EcoRI - expected fragments:

17869
if there is no Sal in pK2, 10585 ← that is what I need
if 6905 contains BamHI site!
379
there is SalI, then instead of 17869 I will have ~9000
~5869

Wednesday, December 12, 1996.

- 1) Extract maxiprep of Gex (clone 26)
- 2) Extract Wisand Gex (clones 2, 5)
- 3) Prepare vectors and fragments from yesterday,
+ HRP (2) Sal + RI.
- 4) Check 12, 45 with XbaI; 121 + SacII (sequence??)



1950年12月

...no ... in ... Alex 2,5?

225/ Ben + Nde \Rightarrow 1 pr-2 ~~pr-2~~ 500 mab 77

Balance sheet deficit? M.B. there is a deficit

$\rightarrow S \Rightarrow$ Seed $u \in (S)$ and 993
WMP

Enter Bal. II?

It looks like there is 2.10

A small grid diagram with a tree on the left and some handwritten marks.

5. If you explain

P	B	G	1	and	de	to	state	in	the
---	---	---	---	-----	----	----	-------	----	-----

[illegible]

→ Bilateral (7 ex)

PTGins for EORI → 8% (10%) (0.1/10)

3. ~~Given~~ 49 kg ~~of~~ $\text{Fe} + \text{R} \rightarrow \text{A} + \text{B}$ (40 kg) (0.1/1.0)

Fluorper 10 µl vekt + 10 µl 11 serf

72. $10 \mu\text{l vect}^r + 10 \mu\text{l H}_2\text{O} + 1 \mu\text{l RT} + 1 \mu\text{l Ligase}$

Thursday, December 12, 1996

1) Take 626 p. acid from C & Cl. - E + Br \rightarrow 2nd spin

2) Extract 223 WHP (42, 48 - didn't grow)

3) Transform ^{and} ligation mix from yesterday, why? 4)

4) Split 293 cells

5) Transforms 42, 45 make NMP maps immediately!!

Seed 42, 45 again → to diff this time!

Need to sequence all 45 need WMA

2) Grow up so $(C_A + A/DPI) \rightarrow$ Ready for construction

1990

0000

Friday, December 12+1, 1996.

- 1) Purify 626 from cell.
- 2) check amount of ~~cal-01~~ fragments ~~plasmid~~ ~~cal-01~~ fragments ~~plasmid~~

Saturday, December 14,

- 1) Prepare LB, sterile eppendorffs, sterile TE, ~~sterile~~ ~~LB~~
- 2) Dissolve 626 prep in sterile TE. ~~check~~ ~~plasmid~~ with ~~plasmid~~
- 3) Split 293 cells to ~~transformation~~ ~~626+~~ ~~left~~
- 4) Repeat transformation of ~~old~~ ~~prep.~~ ~~at~~ ~~cells~~
- 5) Transform DMSO (new) prep with 42, 45, ~~plasmid~~

Tex, 7c \Rightarrow 10 μ l of each to 100 μ l of old DMSO cells.

42, 45 \Rightarrow 0.001 g of each to 100 μ l of new DMSO cells.

Monday, December 16, 1996.

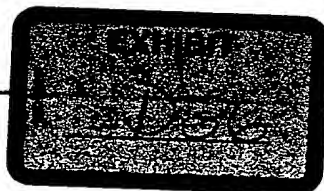
Tex, 7c \Rightarrow no clones again, efficiency of transform is ~~pretty~~ ~~high~~.

What's wrong? Ligation? $10^4 \times 10^3 \approx 10^7 / 1 \mu$ g pL1 $\Rightarrow \approx 10^8 / \mu$ l ~~plasmid~~
Not optimal ratio vector/insert (?)
pBSK was pBSKS (?)

- 1) Dissolve 626 ~~in~~ ~~sterile~~ ~~TE~~, check on EIE amount and quality of the plasmid, check other plasmid as well. (left over)
- 2) Transformation of ~~293~~ with 626+ left over.
- 3) Ligate Tex again, transform DMSO, 5 μ l vector transform CMV/TTF1. 15 μ l insert.
- 4) Seed 42, 45 to liquid culture (LB).



22-141 30 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



60r

pRRV - left arm plasmid (4.5 μ l) 7 μ l (10 \times)
 pBB2 - (PUC119 derivative) (0.58 μ l) 100 μ l (50 \times)

✓ 1.5 ml 2X HEBB

✓ 1200 μ l H₂O.

✓ DNA (107 μ l)

✓ 150 μ l CaCl₂.

✓ 3 ml \Rightarrow for 6 drops

2X Overlay

(for 100 ml overlay)

50 ml 2X DMEM

5 ml 7.5% NaHCO₃

2 ml FCS

1.3 ml 1.8% Noble agar.

Tuesday, December 17, 1996.

7ex \rightarrow no clones. Something in fragment preps. interfere with ligation? (It's possible, because of this red colour stain)

1) Seed iCMVITTE, 54 (L2 + ADP) into large scale liquid culture LB.

ii) TK (31) \rightarrow small scale liquid culture \rightarrow WMA.

2) Extract 42, 45 with Wizard mini prep, 4th, 5th, seed 42, 45 for medium scale prep.

3) Try precipitate fragments 140/SR, 31 SR to purify them.

4) Try partial digestion p223 Bam Nde (Nde - complete, Bam HI - partial dephosphorylate, try cloning with 140 B N

Try to clean Wizard clean up with clean up system.

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



Wednesday, December 18, 1996.

Thursday, December 19, 1996

Cut pFG140 → (Bam + Nde) (buffer D)

Sal I + Eco RI (buffer D)

Cut 223 with Nde → then with Bam HI (partial) →
(complete)

→ ~~plasmid~~ → CLP → vector from gel.

Cut 31 with Sal + Eco RI (buffer D)

Cut 223 Eco RI (buffer D)

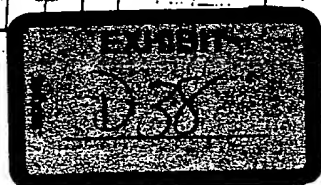
31/R, 1no/R, 223 Nde, 223 R, 1no/Bam Nde

Sunday, December 22, 1996.

- 1) Overlay dishes 293 with neutral red.
Split 293 cells to dishes → repeat transfection.
Seed frozen 293 cells for later passage.
- 2) Check 31, 31/Sal, 31/R, 31/Sal + R to estimate
molecular weight of the plasmid, 223/Nde, and partial
with Bam HI.
- 3) Cut fragments from gel, ligate.
- 4) Seed CMV/ITF, 59 for large scale liposome culture LB.
- 5) Seed Φ plasmid for WAP.

Sunday, December 29, 1996.

- i) CMV/ITF - with Pst II, Sac I.
- ii) pTK? → Kluvin + Xba I, Pst I.
- iii) p54 (rap) - Pst I.
- iv) 42 - Xba I
45 - Xba I } 2% agarose.



- * 2) Split 293 cells to dishes for transfection.
 3) Cut 1101/1107 DNA with *EcoRI*.

Transfection:

- 2 dishes pFG110.
 → 2 dishes E1 + pBAG11
 → 2 dishes E1 + pBAG11 dEGpr CMV from his.

First attempt
 to make KO1
 12/04/96 (T)

500 μ l 2x HEBs + 450 μ l H₂O + 20 μ l pFG110.
 + 1 + 20 μ l BAG11
 + 1 + 20 μ l BAG11 (EGpr CMV) + 10 μ l GCL

Precipitate is coarse
 arginine where E1 plasmid is used \Rightarrow purify it (SCE binding)

Saturday, December 4, 1997.

- 1) Cut 1101/1107 with *EcoRI*.
 → 2) Split 293 to dishes, cotransfect 1101/1107 with L2
 → 3) Pick up this ugly things resembling plaques + to plate to try to grow up + plaques
 → 4) Overlay dishes with NR.

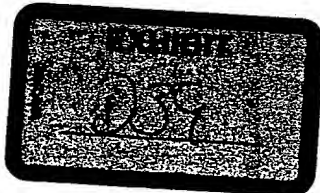
Overlay 2x 200 μ l

200 ml 2x DMEM
 4 ml 2x PS
 4 ml 5% yeast extract.
 3 ml FBS
 10 ml HS
 2 ml 100x chloramphenicol
 20 ml bicarb 7.5%.

Transfection. 1101/1107 /RT + control (his)
 2(x) + L2 (20x)
 + 54 (20x)

4 ml of each transfection mixture

2 ml of 2x HEBs.
 1.8 ml of H₂O
 DNA
 + 200 μ l GCL 2.5M.



Wednesday, 8, 1996.

- 1) Spin left hand plasmid in ~~fast~~ gradient 2x time.
- 2) Split 238 to dishes for transfection.
- 3) Cut 31 with EcoRI \rightarrow complete digestion and with Sal I \rightarrow fragment dephosphorylate.
- 4) Cut 225 (21 + SPB prom) / Mde with Bam HI partial \rightarrow dephosph.
- 5) Fragments (no Sal + Mde, Bam + Mde \rightarrow cut from gel,
- 6) Ligate. 7ex, 10ex overnight.
- 7) Precipitate 1101/1102 DNA end time, cut with EcoRI!
- 8) Sequence 42.
- 9) Run experiment with TK gene.

Thursday 9, 1996

- 1) transform Kurt's left-hand plasmid

Monday, 14, 1996.

transfection $5 \times \text{loc 2} (5 \mu\text{l}) + 15 \times \text{B2B} (15 \mu\text{l}) (1:3)$
 or $10 \times \text{loc 2} (10 \mu\text{l}) + 10 \times \text{B2B} (10 \mu\text{l}) (1:1)$
 or $5 \times \text{loc 2} (5 \mu\text{l}) + 20 \times \text{B2B} (20 \mu\text{l}) (1:4)$

Ligation 8ex 225 / Mde + Bam (partial) CIP
 + 140 / Bam Mde B fragment

Thursday, 17, 1996.

- 1) Sequence 42, primers (a) 4, (b) 5 \rightarrow

\Rightarrow sequence \Rightarrow 42, 1510s

\Rightarrow No sequence at all!
 What is it?

EXHIBIT

D40

8^{pl} premix
 3^{pl} p42
 7^{pl} primer (4 or 5)
 8^{pl} H₂O

circ. long

Monday, 20, 1996.

8 ex (p223 / complete hydr. Nde + Partial Bam)
 (+ B fragment pFG140 / Bam + Nde.)

Miniprep 5; 8 ex (1-12).

- 1) Ladder.
- 2) p223.

3) →
 clones 8 ex 1-12.



- 1) Ladder
- 2) pFG140 / Bam + Nde
- 3) p223 Bam + Nde.
 (upper fragment -
 because of incomplete
 Nde digestion)

4) 81

5) 82

6) 86

7) 87

8) 88

9) 89

10) 810

clones (82, 86, 87,

Nde +
 + Bam

EXHIBIT

D41

22-141 50 SHEETS
 22-142 100 SHEETS
 22-144 200 SHEETS



Cloning 9ex

⇒ 82 / ~~82~~ XbaI - vector 1 fragment
 18 kbp
 18 fragment ~ 9 kbp

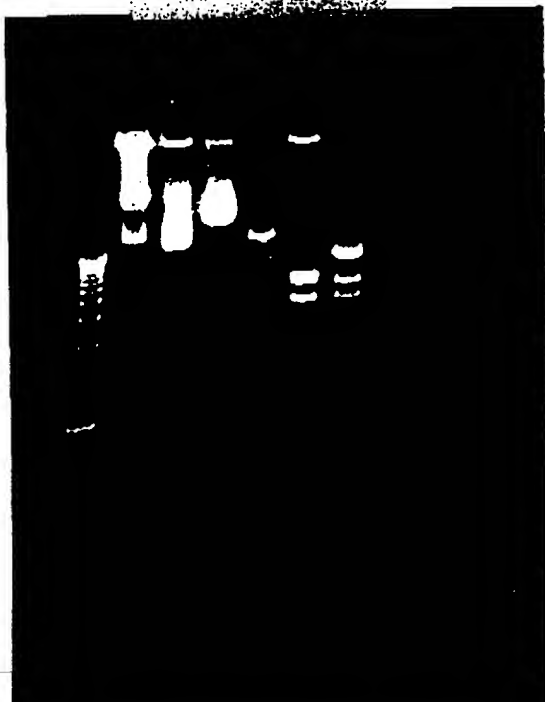
insert p31 / EcoRI + XbaI - 1 fragment

~~Don't use every 1~~ ~~Not XbaI XbaI~~
~~but XbaI XbaI~~

ligation vector 82 / XbaI Afr. 5' (0.1 / 10)
 insert 31 / XbaI Afr. 5' (0.1 / 15)
 +
 2 μl H₂O.
 2 μl Buffer.
 1 μl Ligase.

2 X 82 prep. of 82

- 1) Ladder.
- 2) 240
- 3) 223
- 4) 82
- 5) 110
- 6) 225 / 180 + 110
- 7) 82



11/12

January 25, 1997.

g c and gex \rightarrow ~100 bad colonies / dish
in both cases \Rightarrow (check plasmid vector)

Transfection : 1101/1107/ScRI (0.5 r/ μ l)
 + pK82 (E4 \rightarrow SPB) (10 r/ μ l)
 + CMV/TTF (2 r/ μ l)

10 6cm dishes: 4 control + 6 experiment

1) control A) 8 μ l (4 r) 1101/1107 (1 ml precip)

2) control B) 8 μ l 1101/1107/ScRI + 5 μ l CMV/TTF \Rightarrow (4 r) (10 r)
 \Rightarrow control on wt and toxicity of TTF.

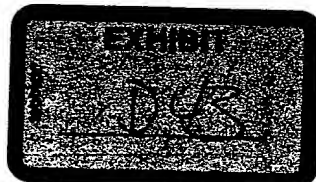
3) exp. 8 μ l (1101/1107/ScRI) \Rightarrow 4 r

A) + 10 μ l p82 \rightarrow 10 r.
 + 3 μ l CMV/TTF \Rightarrow 6 r

B) 8 μ l 1101/1107/ScRI \Rightarrow 4 r
 + 5.0 μ l p82 \Rightarrow 5 r
 + 5 μ l CMV/TTF \Rightarrow 10 r

C) 8 μ l 1101/1107/ScRI \Rightarrow 4 r
 + 15 μ l p82 \Rightarrow 15 r
 + 1 μ l CMV/TTF \Rightarrow 2 r

22-141 50 SHEETS
 22-142 100 SHEETS
 22-144 200 SHEETS



Sunday, February 2, 1987

Transfection

8 large dishes.

2 - 626 + 602 (left-hand)

2 - 41 + 602 (left-hand)

2 - 1101/1107/RT - control + CMV/ITR

2 - 1101/1107/RT + p82 + CMV/ITR

400 RNA for 2 ml of precipitate - each dish

(626) 4 ml of precipitate \Rightarrow

\Rightarrow 2 ml NEBS 2X + 100 μ l 602

p602 = 80 μ l (40x) \checkmark 2 ml H₂O

p602 = 40 μ l (40x) \checkmark

(41)

p41 = 40 μ l (40x) \checkmark

p602 = 40 μ l (40x) \checkmark

(82 - control) \checkmark 1101/1107/RT - 25 μ l (12x)

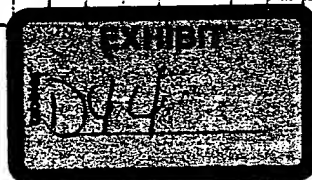
\checkmark pCMV/ITR - 20 μ l (40x)

(82 - exper.)

\checkmark 1101/1107/RT - 25 μ l (12x)

\checkmark pCMV/ITR - 20 μ l (40x)

\checkmark p82 - 30 μ l (40x)



Wednesday, February 5, 1997

Transfection of esi with 626 + LacZ (Koban's with ITR)
~~626~~ + LacZ (— a —)
 626 + LacZ (Good's pAUS4...)

626 + M

2 ml HEBs 2X + 2 ml H₂O + 100 μ l Gd₂

✓ p 626 - 100 μ l (500)

✓ phorbol's - 5 μ l (80)

67 + M

✓ p DUG 11 - 50 μ l (500)

✓ p phorbol's - 5 μ l (80)

626 + C

✓ p 626 - 100 μ l (500)

✓ p AUS4 - 20 μ l (200)

TTC TCTAGA AGT... ATGA GATCTAGA

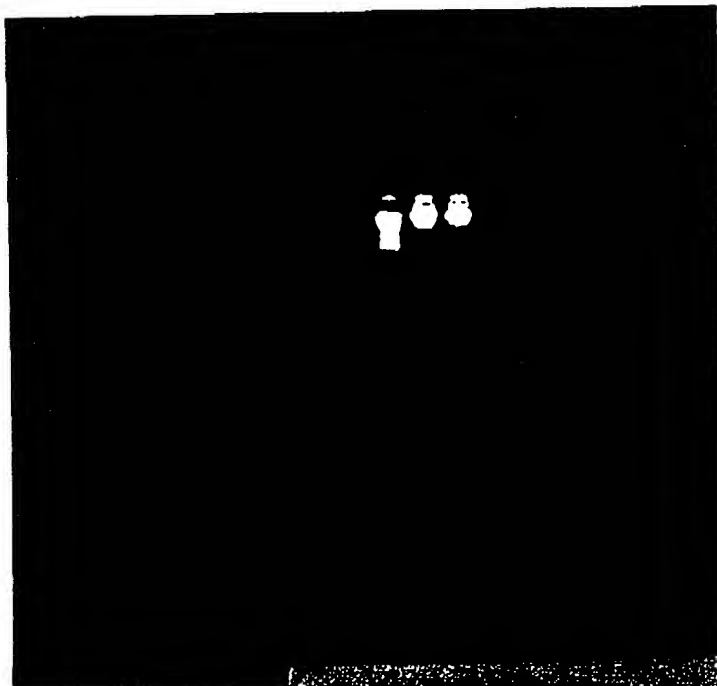
1) ladder

2) - 42 / X6

3) - 45 / X6

⇒ linear form

2nd X6 in the
 plasmid is methylated!

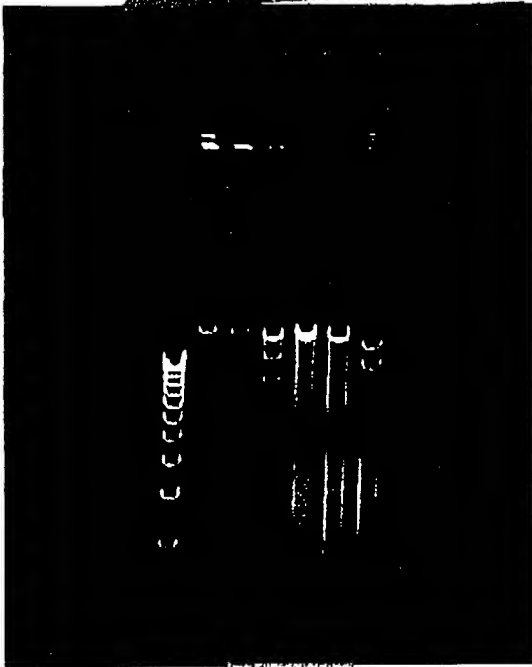


EXHIBIT

D45



Sunday, February 9, 1997



Analysis of 11011102 (R1)
 54
 plagues 54-2

1) Coldder.

2) 11011102 Pcc 1
 3) 11011102 Pcc 1 + Bann H
 4) 11011102 Pcc 1 + Bann H

5) 54-2

6) 54-2

7) 54-2

Pcc

Pcc + Bann H

Conclusion 54-2 - wt
 but there are
 additional bands

PCR, primers
 (D1, K1) 5

1) Coldder

2) DFG 140

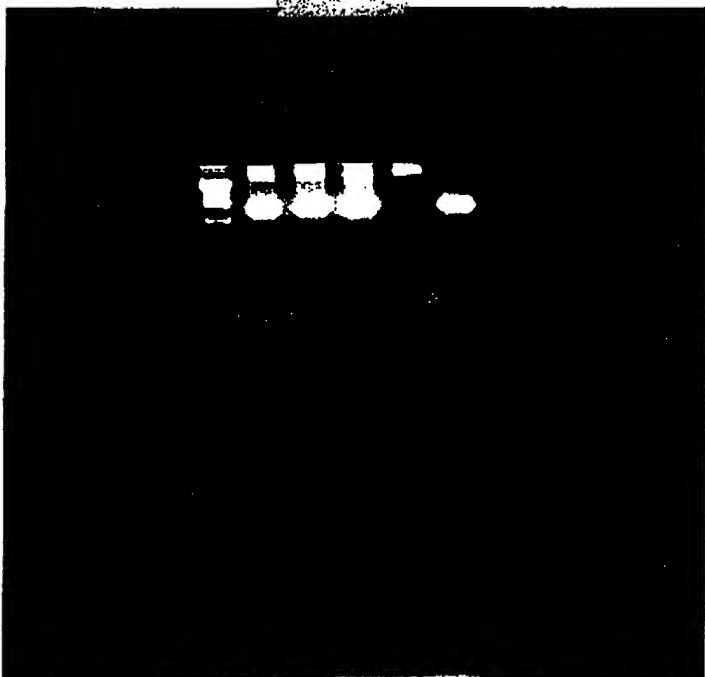
3) p82

4) p54

5) plagues 54-2

Conclusion -

54-2 → wt 63.



February 10, 1997.

Transfection of Mohan's 293/CNV/ITF with p82.

Control : 50 μ l of 1101/1107/EcoRI (10x)
 + 20 μ l pCNV/ITF (20x)
 + 100 μ l p82 (100x)

3 ml H₂O
 3 ml HEBS 2X
 300 μ l CaCl₂ 2.5M.

p82 50 μ l 1101/1107/R1.
 + 20 μ l pCNV/ITF
 + 100 μ l carrier DNA

February 11, 1997.

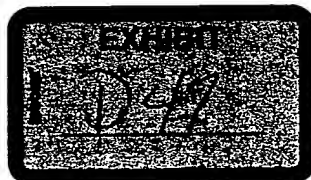
Repetition of ex. vector \rightarrow CIP \rightarrow Heat inactivation

92/R1-K6 (vector) - 5 μ l -
 31/R1-K6 (insert) - 10 μ l
 Lig. buffer - 2 μ l
 ligase - 1 μ l.

February 14, 1997.

Transfection with 1101/1102/EcoRI + or pL2
 p54 (L2+ADP)

Cont A	10 μ l 1101/1102/EcoRI (5x)	+ nothing
Cont B	-----	+ 30 μ l carrier (30x)
L2 A	-----	+ 30 μ l L2 (30x)
L2 B	-----	+ 30 μ l L2 (30x)
54 A	-----	+ 50 μ l 54 (25x)
54 B	-----	+ 50 μ l 54 (25x)

1 ml HEBS 2X + 1 ml H₂O + 100 μ l CaCl₂.

Cloning experimental 9 (9x)

with new vectors 82 / λ G + K1 (1)

82 / K1 + λ G (2)

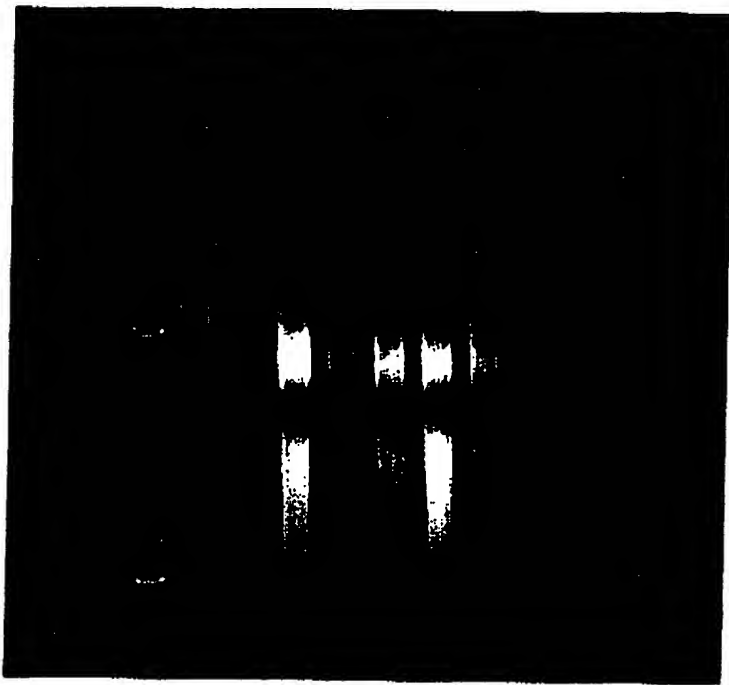
C vect 0.1/5 site ~ 10%

C insert 0.1/5 ~ 2%

9 ex 1 - spl vect + spl insert

9 ex 2 - spl vect + spl insert

February 20, Thursday



Analysis of
restriction
pattern of
plasmids

1) ladder int.

2) 1107 / Pac I + Bam HI

3) K1 + 7

4) 84-1

5) 84-2

6) 84-3

7) 84-4

8) 84-5

for 84-1

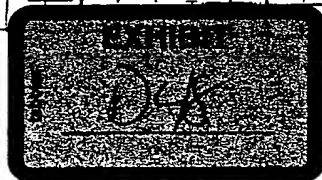
84-3

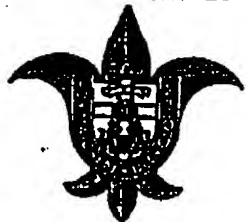
84-4

restriction pattern

is as expected for

recombinant virus





**SAINT LOUIS
UNIVERSITY**

1402 South Grand Blvd.
St. Louis, MO 63104
Phone: 314-577-8432
FAX: 314-773-3403

Department of Molecular
Microbiology & Immunology

Health Sciences Center
School of Medicine

Facsimile Transmittal

Date: 12 - 3 - 02

From: William Wold

Phone: 314-577-8432

Fax: 314-773-3403

Deliver to: Dan Kasten

Phone: _____ **Fax:** 552-76305

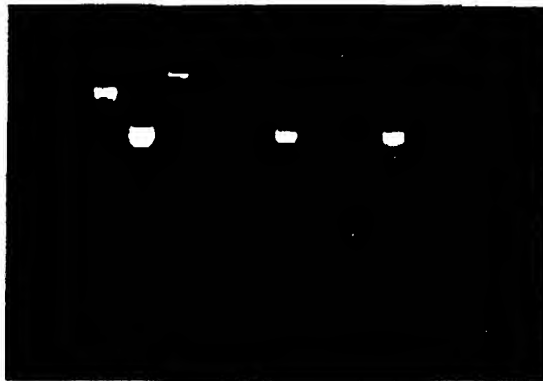
Total number of pages including this page: 12

Message:

Kostya's lab notes.

NO1 is made
2/20/97

2-20-97



PCR of lmt prep
from previous picture
primers 1231 and 1237

- 1) ladder 1ul
- 2) pFG140 (dl 50g)
- 3) pS4
- 4) mock
- 5-9) -
- S4 1-5
- respectively.

viruses S4-2
and S4-5
contain both wt
and recombinant ADP.

there is band as is wt in mock!

S4-1,
S4-3
S4-4 } - recombinants!

02-25-97

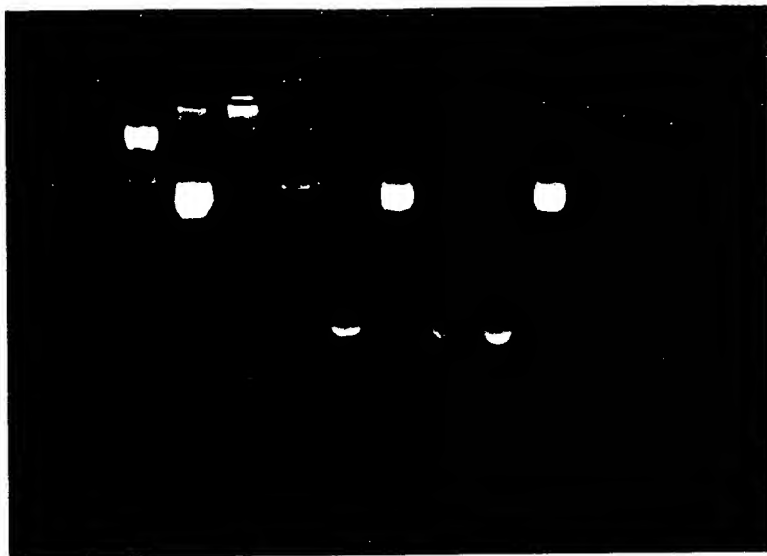
gen. → 2 time purified then gel vector.
p82 / R1 & 6. } 1 fr.
insert p31 / R1 & 6

vector 10ul 82 + 8ul 40 + 2ul buffer

vector lig 10ul 82 + 8ul 40 + 2ul buffer + 1ul ligase

vector + insert 10ul 82 + 8ul insert + 2ul buffer + 1ul ligase
~~vector + insert~~

2.20.93



PCR of int frags
from previous picture.
primers 10D1 and 10D7.

- 1) Gadder 1ul.
- 2) pAG140 (dl scs)
- 3) p54
- 4) mock
- 5 - 9) -
- 54 1 - 5
- respectively.

viruses 54-2
and 54-5
contain both wt
and recombinant ADP!

there is band as in wt in movie!

54-1 }
54-3 } - recombinants!
54-4 }

82 - 25 - 97

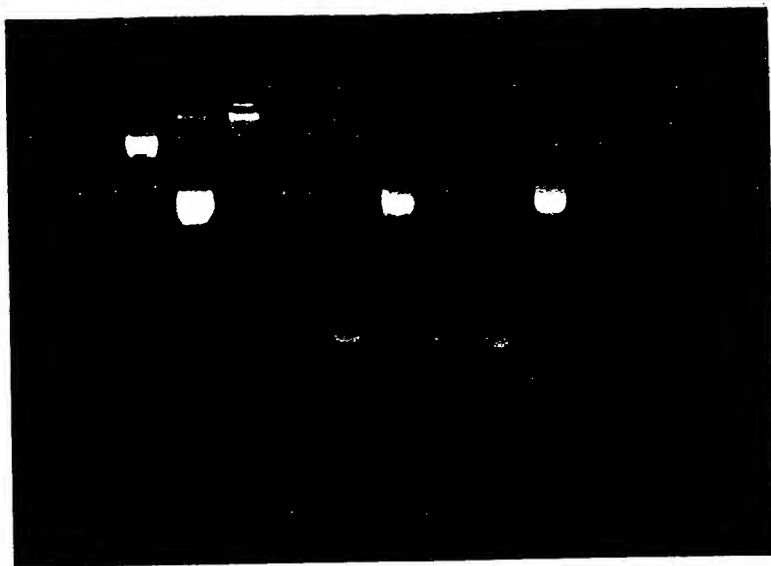
Dec → 2 time purified then gel vector.
p31 / R1 x62 } 11 fr.
insert p31 / R1 x62 }

vector 10 μl 82 + 8 μl H₂O + 2 μl buffer

vector + lig 10 μl 82 + 8 μl H₂O + 2 μl buffer + 1 μl ligase

vector + insert 10 μl 82 + 8 μl insert + 2 μl buffer + 1 μl ligase
~~in 10 μl~~

2-20-97



PCR of *Umb* was
from previous picture.
primers 1 and 7.

- 1) ladder 1ul
- 2) pCG140 (dl 309)
- 3) pS4
- 4) mock
- 5-9) -
- S4 1-5
- respectively.

viruses S4-2
and S4-5
contain both wt
and recombinant ADP!

there is band as in wt in mock!

S4-1
S4-3
S4-4 } - recombinants!

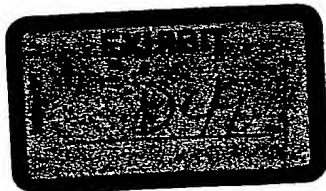
82-25-97

9ex. → 2 time purified then gel vector.
p82 / R1 & G. } 1 fr.
insert p31 / R1 & G.

vector 10 μ l 82 + 8 μ l H₂O + 2 μ l buffer

vector + lig 10 μ l 82 + 8 μ l H₂O + 2 μ l buffer + 1 μ l ligase

vector + insert 10 μ l 82 + 8 μ l insert + 2 μ l buffer + 1 μ l ligase
~~vector + insert~~



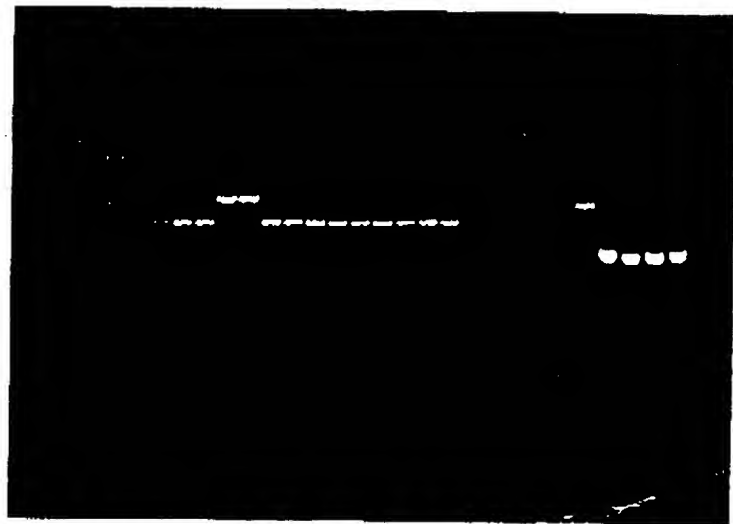
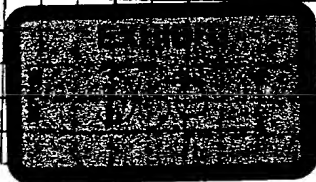
02-25-97

54-10 plaques - phage type that I like

WT + ~~10ex~~ or Rec with high MOI?

Sex - try Str 16?

03-05-97 Wednesday

Clay Experiment 10ex \Rightarrow pL2 + E3 from gp13K (p31)
(sites EcoRI + NdeI).11ex \Rightarrow pL2 + E3 from pE3X66 + ADP
(p42)
(sites \Rightarrow EcoRI + NdeI)PCR analysis
of plaques p82
and p54.

1) Ladder

2) Blank

3) mock

4) 1101/1102

5) PF6/40

6) 825

7) p82

8) wt 1101/1102

9) 821

10) 823

11) 824

12) 825

13) 826

14) 827

15) 8210

16) 8211

primers

10, 11

17) - Ladder

18) - blank

19) - mock

20) 1101/1102

21) PF40

22) 54

23) 546

24) 548

25) 549

26) 5410

primers

1, 4

8

p82 + 1121/1107 / E10R1 plaques!

AC wt 1 - medium size } wt control
AC wt 2 - large size }

transfection
from 01-25

A. 1, (2) - medium.

B. 3 - medium.

➤ 4 - small

5 - medium.

B. 6, 7, 8 - medium

➤ 9 - small

C. - 10. medium.

➤ (11) - small.

(12, 13, (14)) - medium. } p's ones?

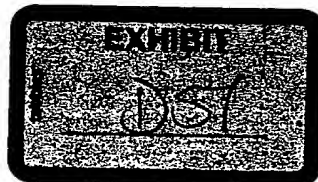
(15) 16, 17 - medium } or not.

transfection
from 02-02

➤ freeze contamination in plate wells

827 > lost due to Rodage of Eppendorf
and 547 > tubes.

⇒ no recombinants with p82 according to PCR results.
p54 = ? ⇒ no product of PCR, just RNA.

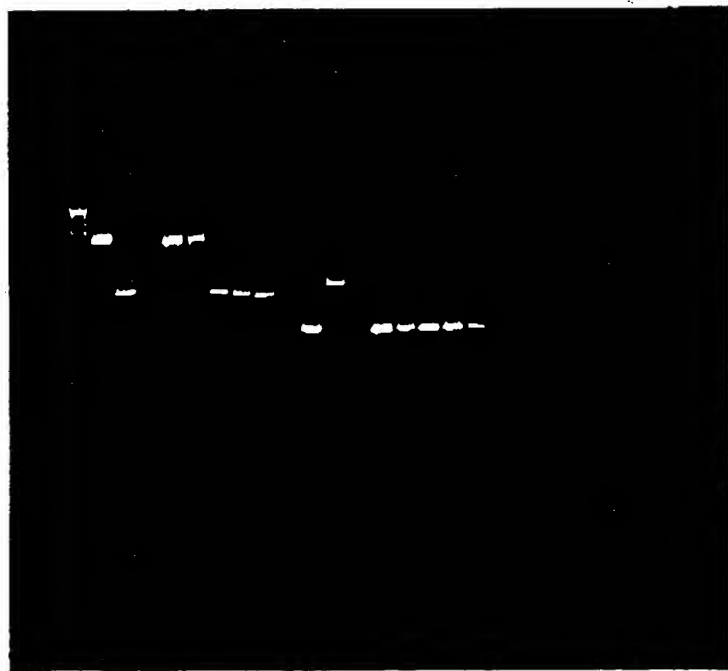


05-06-97

Ligation 10 ex, 11 ex.

5 μ l vector (L2/ENAH) \rightarrow ✓+ ligase \rightarrow VL+ 10 μ l 3' ENL \rightarrow 10 ex L+ 15 μ l 3' ENL \rightarrow 10 ex H+ 15 μ l 4' EN \rightarrow 11 ex

PCR Analysis of plaques



1) ladder

2) 100

3) 54

4) mock

5) WT 1101/1102

6) 546

7) 548

8) 549

9) 5400

10) blank

11) pEG 100

12) p82

13) mock

14) WT 1101/1102

15) 822

16) 825

17) 827

18) 829

primers
40, 1, 7.primers
40, 10, 11.

548, 549, 5410

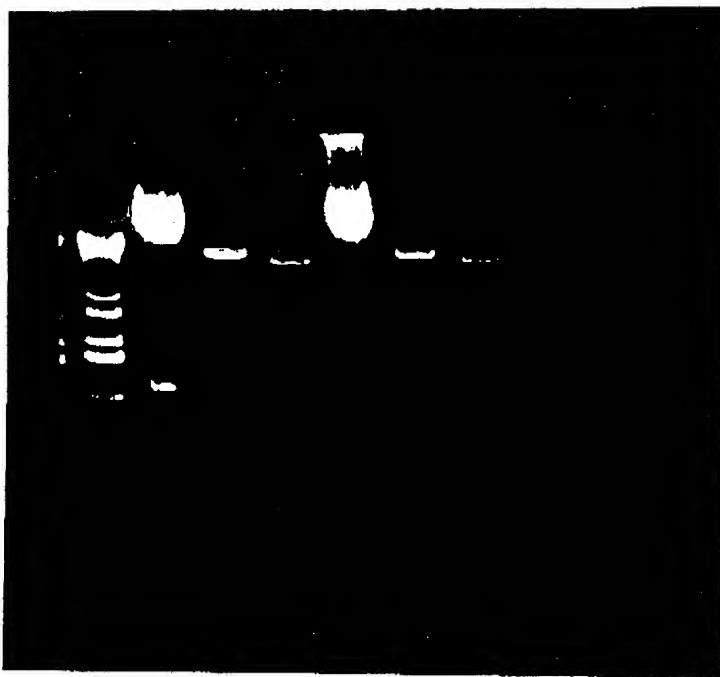
- recombinants

with p82 all
plaques are wt.

EXHIBIT

102

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



- 1) ladder
 - 2) pL2
 - 3) p31
 - 4) p42
 - 5) pL2
 - 6) p31
 - 7) p42
- { EcoRI +
 Nde,
 buffer NE
 { EcoRI +
 + Nde,
 buffer D

03-07-97

Transfection p82 into 293/TTF.

12 dishes — 6 - control (sal of precip.) — 60% DM
 6 - experiment (— — — — —) — 60% DM

(control) 25µl 1101/1107/R1 (50)
 + 5µl penicillin (100)
 + 30µl gentamicin (~300) 1.5ml LIEBS 2X
 1.5ml H₂O.
 150µl CaCl₂

(exper.
 p82) 25µl viral DNA.
 + 5µl penicillin
 + 30µl p82



032 10 - 97

Cloning 10 ex. 41 ex.

1 - ladder

2 - p42

3 - p31

4 - p42

5 - 10L-1

6 - 10L-2

7 - 10L-3

8 - 10L-4

9 - 10L-5

10 - 10L-6

11 - 10L-7

12 - 10H-1

13 - 10H-2

14 - 10H-4

15 - 10H-5

16 - 10H-6

17 - 10H-7

18 - 10H-8

19 - 11-1

20 - 11-2

21 - 11-3

22 - 11-4

23 - 11-5

24 - 11-6

25 - 11-7

26 - 11-8



19 - all clones - rect 15

10H - all clones - recant hunk
lower land was visible in
all clones in short runTake 11H and 10J
per GSC Maps.

Eucali + Mest

EXHIBIT

1054

03-12-97

hint traps of small amount (plate) of 293/TTC
infected with slow growing viruses p82(?)
PCR, primers 10, 11.

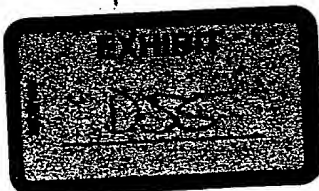
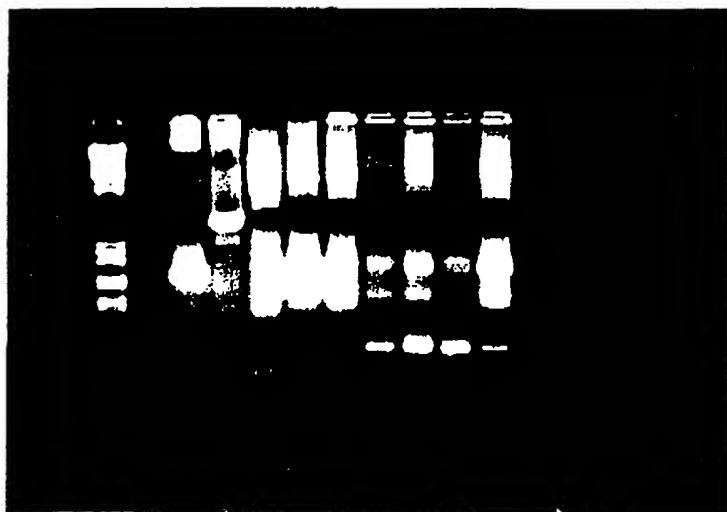
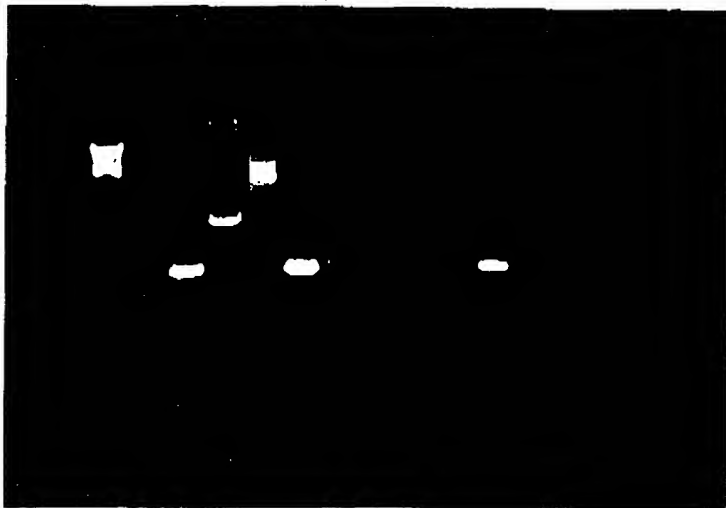
- 1) ladder.
- 2) blank (H₂O)
- 3) pR611uo.
- 4) p82
- 5) mock.
- 6) wt.
- 7) 8212
- 8) 8214
- 9) 8215
- 10) 8216
- 11) 82-17

Conclusions:

blank. clean.

in 82-12, 82-17 -
band, corresponding to wt.
and weak additional
band corresp. to rec.
(does not present in wt!!!)
something of a bit smaller
MW present in mock.

22-141 50 SHEETS
22-142 100 SHEETS
22-143 200 SHEETS



3-07-97

PCR analysis of p82 resulting plaques / primers

w/ 8, w/ 9 -

- SPB - promoter
specific.

1) ladder

2) blank

3) pG140

4) p82

5) mock

6) wt 1.04/1.107

7) 821

8) 822

9) 823

10) 824

11) 825

12) 826

13) 827

14) 828

15) 829

16) 8210

17) 8211

18) 8212

19) 8214

20) 8215

21) 8216

22) 8217

On cloning there is SPB in 293 cells,
viruses are rather w/ than
recombinants, need to use

(12) 8, (14) 4 combination of primers / 8 - SPB specific

3-18-97

Sequencing

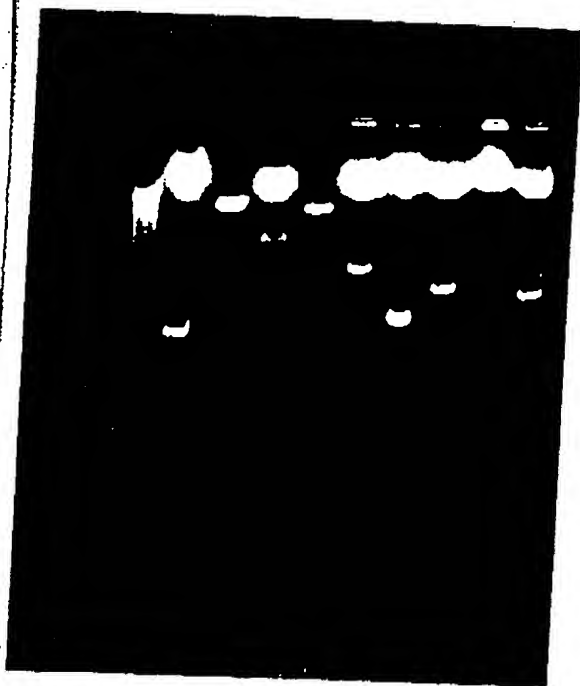
KD 9 (p 21 , primer KD10)

KD 10 (p 21 , primer KD11)

KD 11 (p 111 , primer KD4)

KD 12 (p 111 , primer KD5)

Restriction pattern of Csl preps. of p101, p111



- 1) 1 kb ladder
- 2) L2 / R1 + NdeI
- 3) p31 / R1 + NdeI
- 4) p101 / R1 + NdeI
- 5) p42 / R1 + NdeI
- 6) p111 / R1 + NdeI
- 7) L2 / PacI + SpeI
- 8) p101 / PacI + SpeI
- 9) L2 / SpeI + XbaI
- 10) p111 / SpeI + XbaI

3-21-97

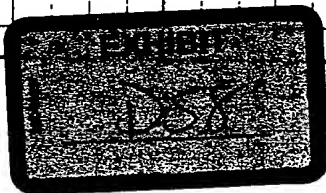
Analysis of sequences KD 9, 10, 11, 12.

Everything is fine with p111. As predicted.

p21 - sequence with all primer is fine.

- sequence with KD 10 primer shows that the
 E. coli sequence is going after Ad nt 35858 and
 up to the end of sequence (approx 500 kb) → see

⇒ p626 and p82 are not responsible for virus
Need to check p54611 for the same mutation.



Lakes K03

3/27/97

3-20-97 Regues. (experiments of 02/05)

626M 1-12 (12)

626C 1-6 (6)

11M 1-4 (4)

3-25-97

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

1) ladder 1kb

puffer-Mc

2) 1101/1107 DNA / EcoRI + SpeI

3) p82

4) p82 / Bst 1107 I

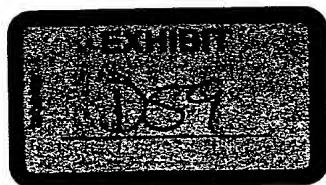
5) p82 / XbaI

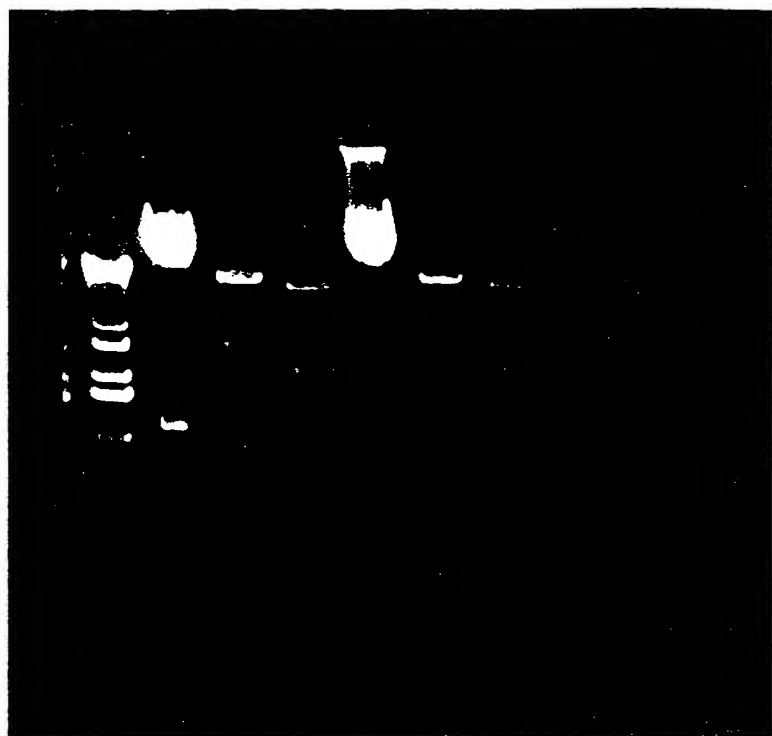
6) p82 / Bst 1107 I + XbaI

There is Bst 1107 I site at A129012!

2nd is after SSB powder!

3-27-97

Transfection 293 with p101, p111 + 1101/1107 / EcoRI + SpeI
8X Gen dishes.3 dishes 101 (for 1 dish) 200 µl KES2X + 200 µl H₂O + 10 µl 1013 dishes 111 (for 1 dish) 200 µl KES2X + 200 µl H₂O + 10 µl 1112 dishes control (for 1 dish) 200 µl KES2X + 200 µl H₂O+ 10 µl 1101/1107 + 25 µl CaCl₂.



1) ladder

- 2) pL2
3) p31
4) p42
- 5) pL2
6) p31
7) p42
- EcoRI +
Nde,
buffer ME
- EcoRI +
+ Nde,
buffer D

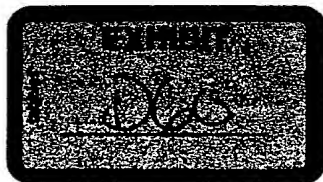
03-07-97

Transfection p82 into 293/TTR

12 dishes — 6 - control (3rd of precip) — 60% DNA
6 - experiment (— — — — —)

(control) 25 μ l 1101/1107/R1 (50)
+ 5 μ l penicillin (100)
+ 30 μ l buffer (~300) 1.5 ml LIEBS 2X
1.3 ml H₂O
150 μ l CaCl₂

(exper. p82) 25 μ l viral DNA
+ 5 μ l penicillin
+ 30 μ l p82



03410-97

Cloning 10 ex, 11 ex.

1 - Colder

2 - p42

3 - p31

4 - p42

5 - 10L-1

6 - 10L-2

7 - 10L-3

8 - 10L-4

9 - 10L-5

10 - 10C-6

11 - 10C-7

12 - 10H-1

13 - 10H-2

14 - 10H-4

15 - 10H-5

16 - 10H-6

17 - 10H-7

18 - 10H-8

19 - 11-1

20 - 11-2

21 - 11-3

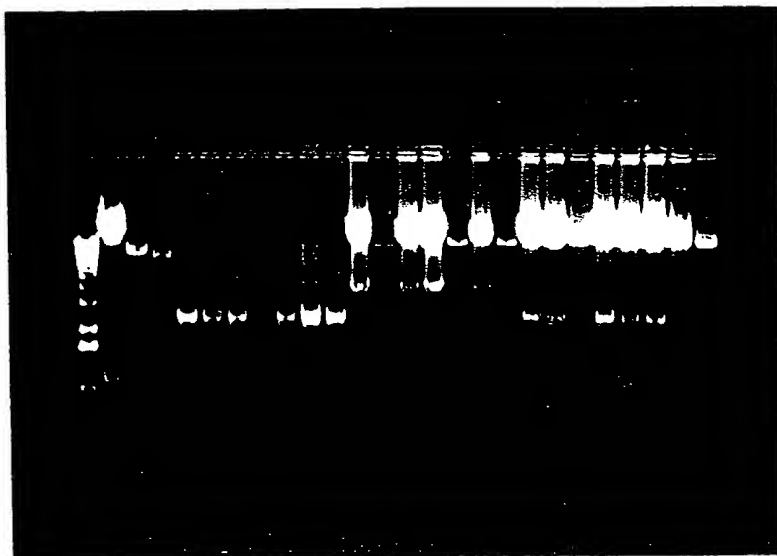
22 - 11-4

23 - 11-5

24 - 11-6

25 - 11-7

26 - 11-8



18 - all clones - rect 15

10H - all clones - recontaminated
lower band was visible in
all clones in short run.

take 11 and 101
for cell prep.

Enoki + Nde I



03-12-97

Hint maps of small amount (plate) of 293/TTF
infected with slow growing viruses p82(?).
PCR, primers 10, 11.

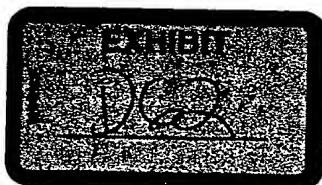
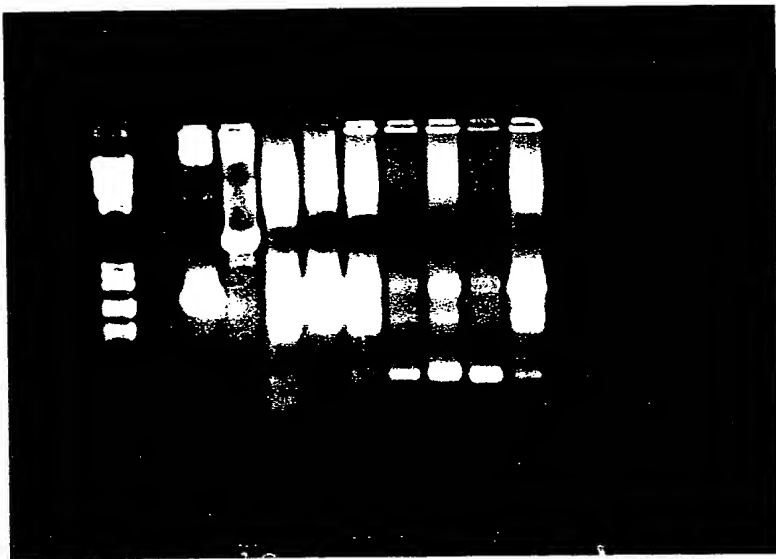
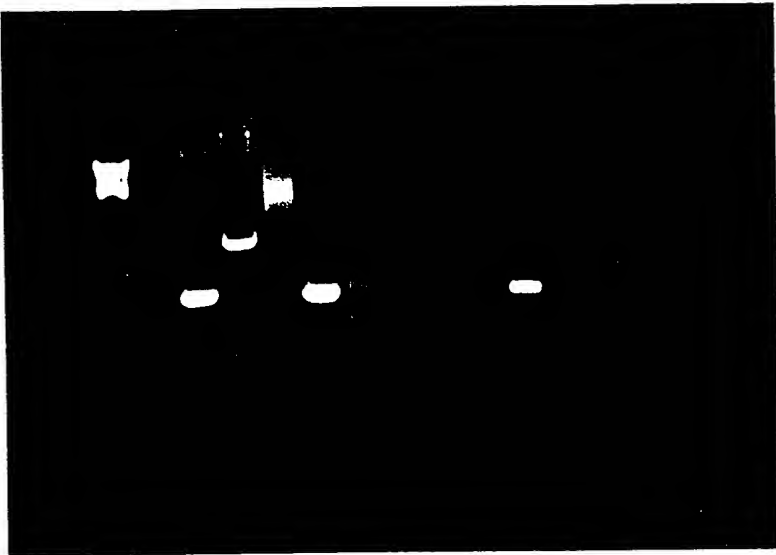
- 1) ladder.
- 2) Blank (H₂O)
- 3) pF6140.
- 4) p82
- 5) Mock.
- 6) wt.
- 7) 8212
- 8) 8214
- 9) 8215
- 10) 8216
- 11) 82-17.

Conclusions:

Blank - clean.

in 82-12, 82-17 -
band, corresponding to wt.
and weak additional
band corresp. to rec.

(does not present in wt!!!
Something of a bit smaller
MW present in mock



3-17-97

PCR analysis of p82 resulting plaques & primers

wd 8, wd 9 -

- SPB - promoter -
specific).

1) ladder.

2) blank.

3) pFG140.

4) p82

5) mock.

6) wt 101/1107

7) 821

8) 822

9) 823

10) 824

11) 825

12) 826

13) 827

14) 828

15) 829

16) 8210

17) 8211

18) 8212

19) 8214

20) 8215

21) 8216

22) 8217

Conclusion: there is SPB in 293 cells,
viruses are rather wt than
recombinants. need to use

(wd 8, wd 11) combination of primers (9 - SPB specific
11 - AI specific)

3-18-97

Sequencing

KD 9 (p21, primer KD10)

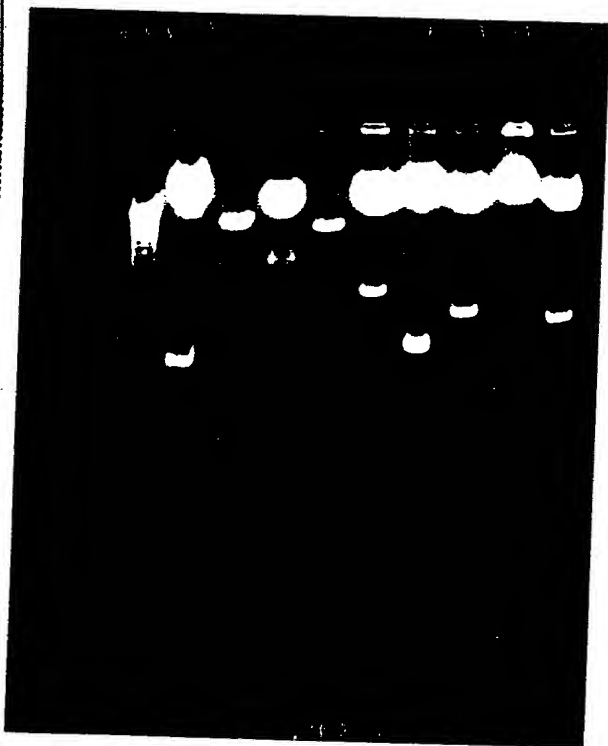
KD10 (p21, primer KD11)

KD 11 (p111, primer KD4)

KD 12 (p111, primer KD5)

Restriction pattern of C₅ prep. of p101, p111.

- 1) 1 kb ladder
- 2) L2 / R1 + NdeI
- 3) p31 / R1 + NdeI
- 4) p101 / R1 + NdeI
- 5) p42 / R1 + NdeI
- 6) p111 / R1 + NdeI
- 7) L2 / PaeI + SpeI
- 8) p101 / PaeI + SpeI
- 9) L2 / SpeI + XbaI
- 10) p111 / SpeI + XbaI



3-21-97

Analysis of sequences KD 9, 10, 11, 12.

Everything is fine with p111. As predicted.

p21 - sequence with all primer is fine.

- sequence with KD 10 primed shows that the E. coli sequence is going after Ad nt 35858 and up to the end of sequence (~500 bp). \Rightarrow see next page

⇒ p626 and p82 are nt resgreble f virus
Need to check p84611 for the same mutation.

3-20-97 Regues. (experiments of 02/05
02/02)

626M 1-12 (12)

626C 1-6 (6)

11M 1-4 (4)

3-25-97

1) ladder 1kb

buffer-ME

2) 1101/1107 DNA / EcoRI + SpeI

3) p82

4) p82 / Bst 1107 I

5) p82 / XbaI

6) p82 / Bst 1107 I + XbaI

There is Bst 1107 I site in p82
at Ad 29012!

2nd is after SPB promoter!



3-27-97

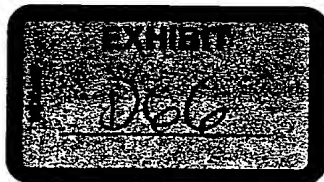
Transfection 293 with p101, p111 + 1101/1107 / EcoRI + SpeI
8x 6cm dishes.

3 dishes 101 (for 1 dish) 250 μ l MEME 2x + 200 μ l H₂O + 10 μ l 101

3 dishes 111 (for 1 dish) 250 μ l MEME 2x + 200 μ l H₂O + 10 μ l 111

2 dishes control (for 1 dish) 250 μ l MEME 2x + 200 μ l H₂O

+ 10 μ l 1101/1107 + 25 μ l GCl₂.





4/7/97

Plaque assay of 544 on 253

309 - (~ 2) - plaques are confluent (no many plaques per dish)
(CCL stock)

1101/1107 (~ 2) - Same as with 309
(CCL and crude ligote)

544 (titer ~ 2 is about ~ 2 orders of magnitude lower than in wt (309, 1101, 1107)
plaques appeared ~ 1 day later than in wt (\sim day 5) and are a bit smaller.

(day 16 size ~ 8 mm)

7001 (CCL) (titer is ~ 2 orders of magnitude lower than predicted for wt)
plaques are tiny (day 16 $\sim 1-2$ mm diameter)

4/8/97

Ligation

12 ex 1) 82 (10 μ l) + PCR product ITR (10 μ l)
Bst (part) + Kba from 140 (49 (6, 17))

2) 87 (5 μ l) +

4/16/97

Ligation 12 ex: vector 87/Kba + Bst (part) + CIP
82/Kba + Bst (part) + CIP
upper fragment
82/Kba + Bst + CIP
lower fragment



4/17/97 Sequencing.

- 14) (14) - (pB4G11, primer KD10)
- 15) (15) - (pB4G10, primer KD10)
- 16) (16) - Nippen's Gd4 large plasmid, primer KD16
- 17) (17) - p82, primer KD10
- 18) (18) - p111, primer KD10.



Link maps of 101-1
and 111-1.

PCR, primers 1,5.

1) Ladder.

2) Blank

3) pB6140.

4) p101.

5) 101-1

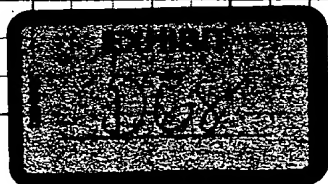
6) p111

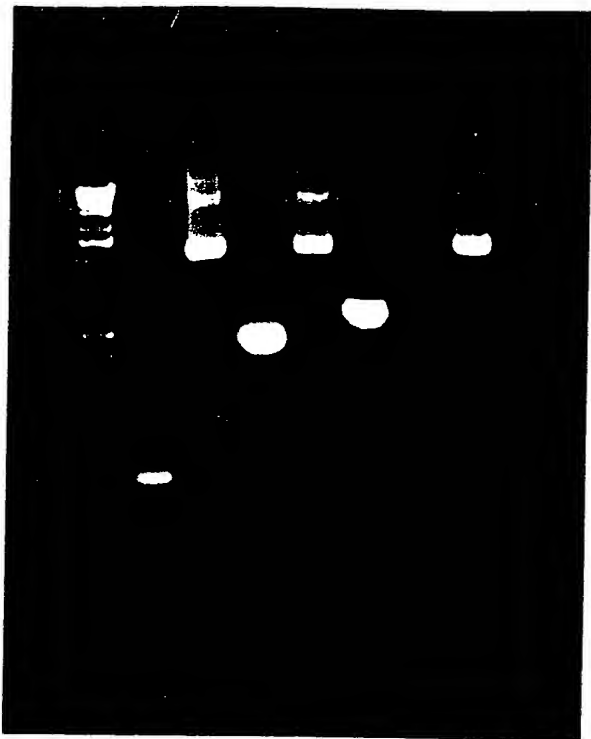
7) 111-1

p101, p111 ⁽¹¹¹⁻¹⁾ BCR didn't work.

for 101-1 product is
as expected for 111

Mixed tubes 10-1, 111-1 → or what?





PCR, primers 1, 7.

- 1) Ladder
- 2) Blank.
- 3) Lys.
- 4) 54
- 5) p101
- 6) p111.
- 7) 101-1
- 8) 111-1.

in 111-1 band is as h wt
(or 101)

in 101-1 band is higher
than wt.

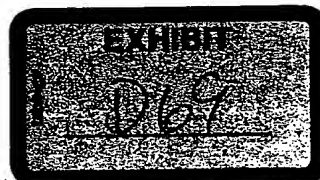
4/21/97

PCR, primers 1, 7.

- 1) Ladder.
- 2) Blank.
- 3) p101.
- 4) p111
- 5) p101
- 6) p111
- 7) 101-1
- 8) 111-1.

Conclusion:
this time everything
is as expected.

- 9) 111-2
 - 10) 111-3
 - 11) 111-4
 - 12) 101-1
- } p6gus.



1/22

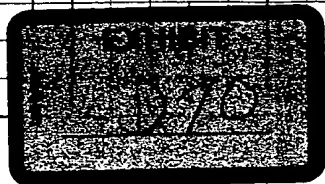
Sequencing

- u) 19 - Chp's pED vector, primer CFC II 6
- u) 20 - pBHG10, primer KD10.
- u) 21 - p82, primer u) 16
- u) 22 - p82, primer u) 17
- u) 23 - p21, primer u) 16
- u) 24 - p21, primer u) 17

Results of previous sequencing:

- u) 14 (pBHG11, primer KD10) - sequence terminates on same point where the sequences start in p21.
- u) 15 (pBHG10, primer u) 10) - same as ↑
primer KD16)
- u) 16 (Mippers large GAL4 plasmid) - same as ↑
but there is some sequence which is what?
- u) 17 (p82, primer u) 10) - sequence of 32-B promoter, need to repeat with u) 16 primer.
- u) 18 (p111, primer u) 10) - sequence is perfect as predicted.

Sequences 19-24 - early termination everywhere
⇒ new protocol doesn't work.





mini preps of 12 ex.

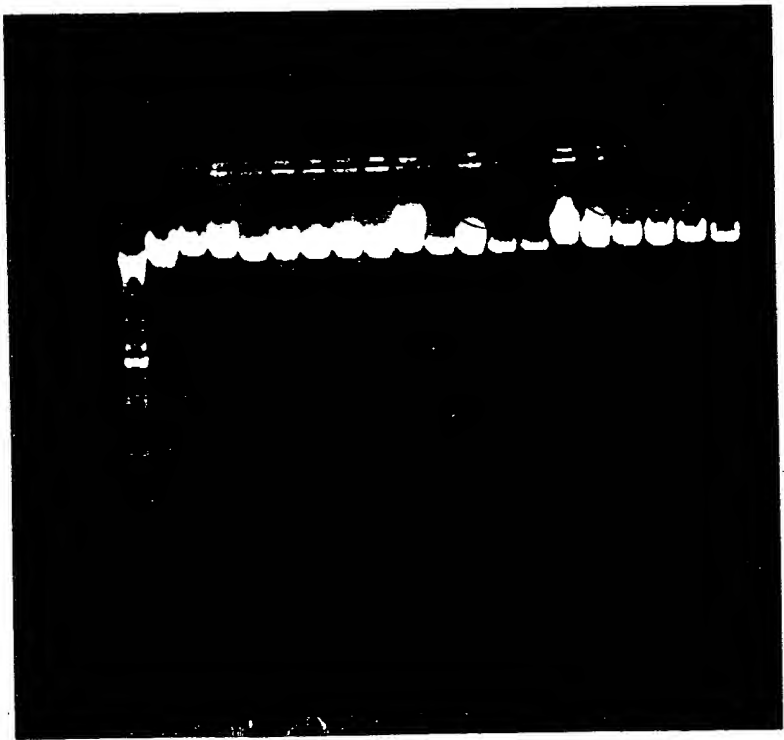
- 1) Ladder,
- 2) p82
- 3) 87-1
- 4) 87-2
- 5) 87-3
- 6) 824ex1 (1-9)
- 7) 824ex2 (1-12)
- 8) ↓
- 9) ↓

- 1) Ladder.
- 2) p82.
- 3) 82L ex1 (1-12)
- 4) ↓ 82L ex2 (1-12)

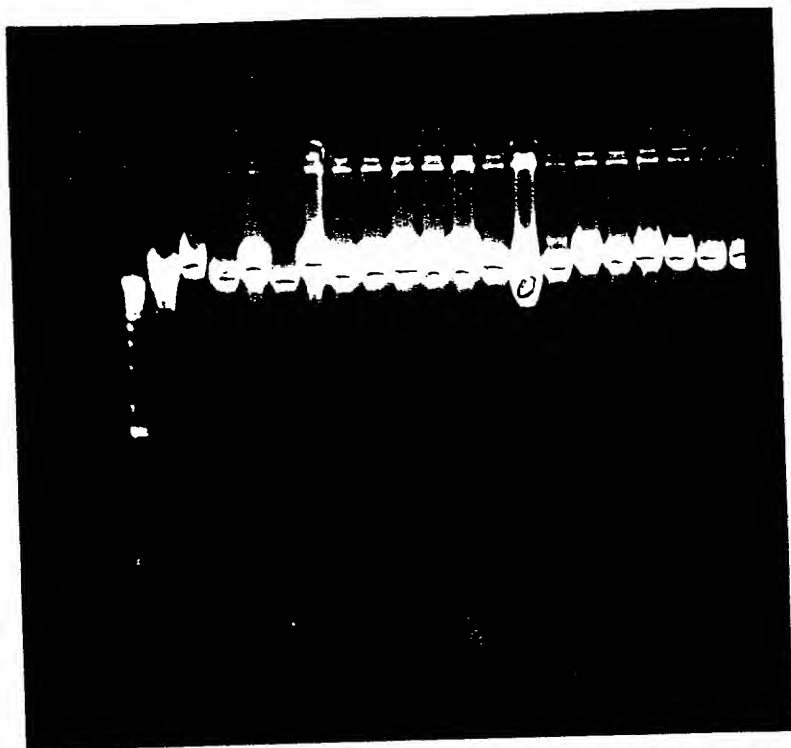
4/23 Restriction analysis of clones 12 ex

- 9) Ladder
- 1) p82 / R1
- 3) p82 / X63
- 4) 871
- 5) 824H
- 6) 824B3
- 7) 8244-4
- 8) 8245
- 9) 446
- 10) 447
- 11) 448
- 12) 449
- 13) 42-1
- 14) 42-4
- 15) 42-5
- 16) 42-7
- 17) 42-8
- 18) 42-9
- 19) 42-10
- 20) 42-12

EcoRI



Conclusions: 82/121 - partial digestion.
clones - no small bands. = 2 possibly recombinants.
Marked bands have lower MW than p82/X63



- 1) ~~adder~~
- 2) p82/R1
- 3) p82/X63
- 4) L1-1
- 5) L1-2
- 6) L1-4
- 7) L1-6
- 8) L1-7
- 9) L1-8
- 10) L1-9
- 11) L1-10
- 12) L1-11
- 13) L2-2
- 14) L2-3
- 15) L2-4
- 16) L2-5
- 17) L2-7
- 18) L2-8
- 19) L2-9
- 20) L2-10
- 21) L2-11
- 22) L2-12

Conclusion: p82 - partial
R1 digestion
clones - no small bands.

L2-3 - exclude from further analysis.

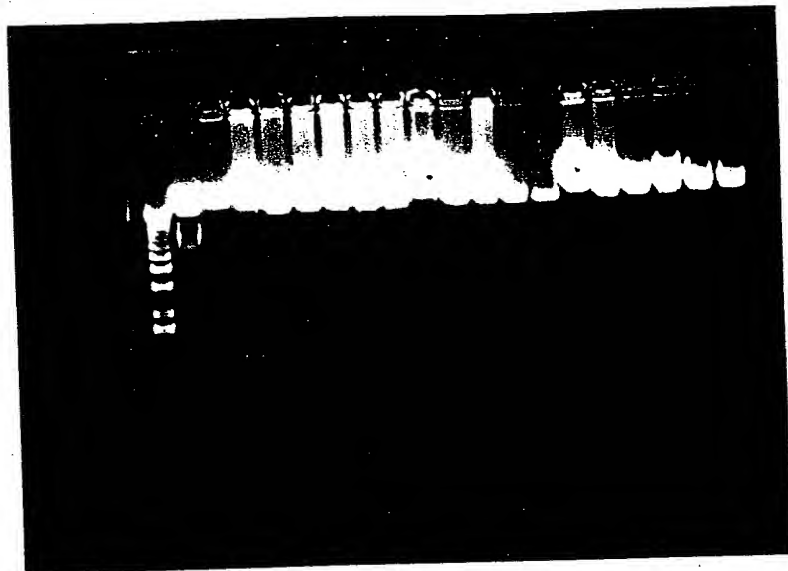
Try NdeI - X63 1 ~~hydro~~ digestion.

expect 5 kb fragment in rec;
6 kb fragment in 82 (wt).

4/29

Same as previous 2
pictures,

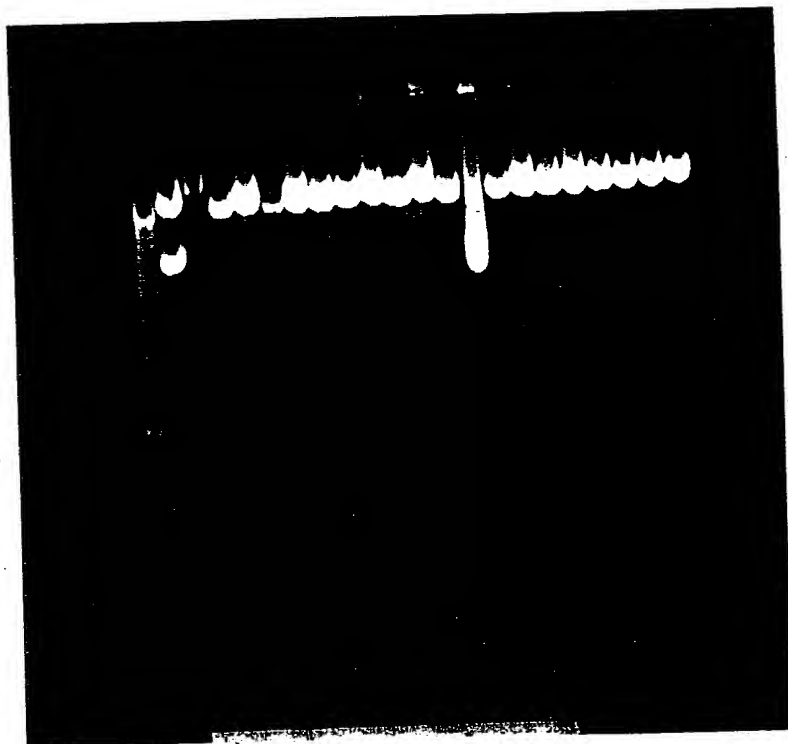
- 1) ladder
 - 2) p82 / Xba + Nde
 - 3) p82 / Nde.
 - 4) clones / Xba + Nde
- ↓



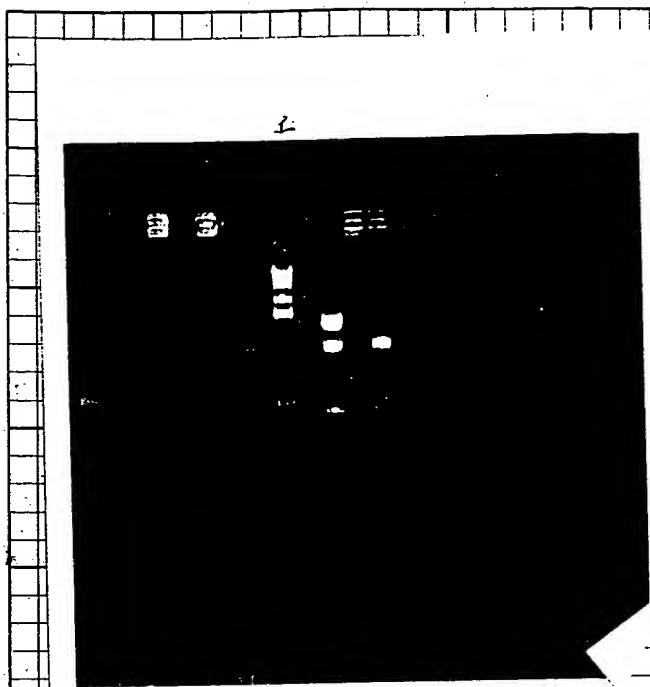
Conclusion of all these
clones are junk,
start cloning of p82
into 223 where Bst
is unique, then put
the resulting plasmid
between Nde fragment from
pRG140 (uniqueness
again).

Probably, most of them
are all Bst - Bst clones?

But where is vector
background?



NDZ is made
4/24/97



4/24

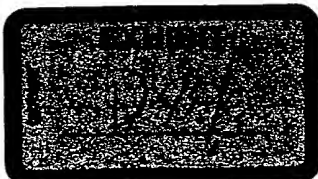
Restriction digestion
of PCR products
with Pst I
(PCR primers 1, 2)

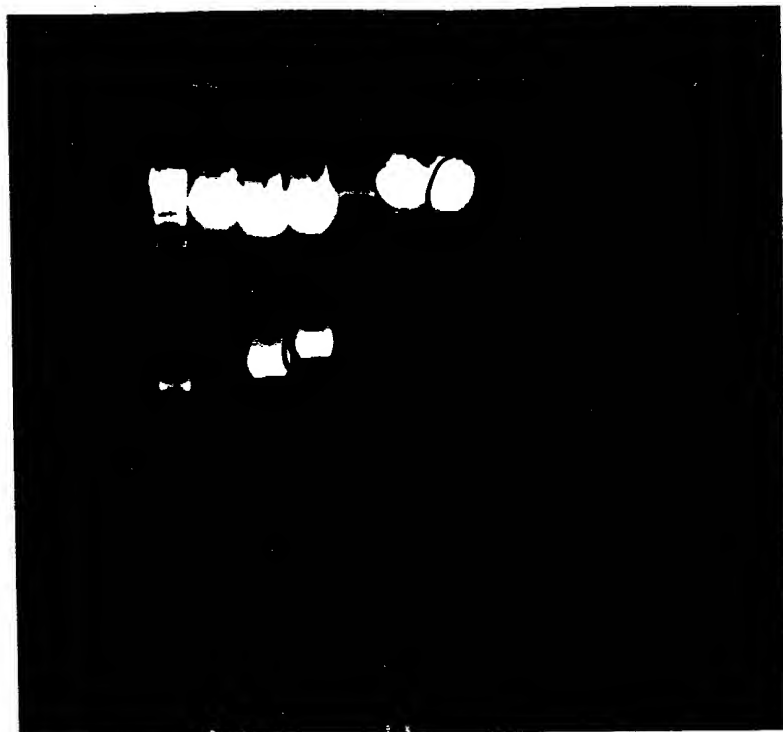
- 1) Ladder
- 2) pGEM
- 3) 101
- 4) 111
- 5) 101-1



- 1) Ladder
- 2) 1101/1107
- 3) 100-1
- 4) 111-1
- 5) 1101/1107
- 6) 101-1
- 7) 111-1

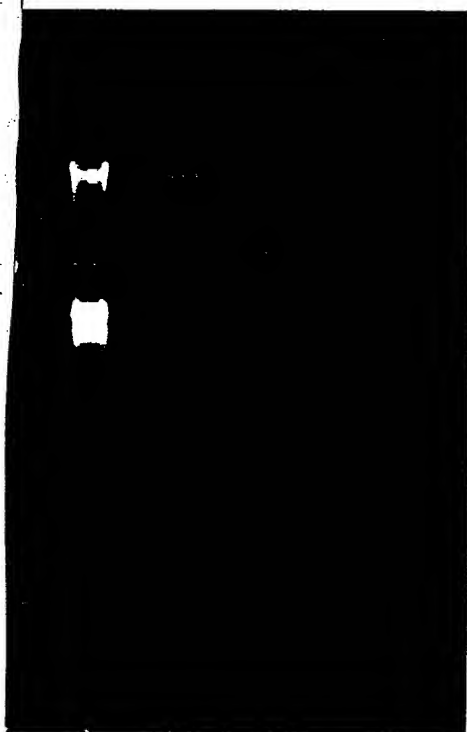
Conclusion: 101-1 is rec.
111-1 ?





4/26.

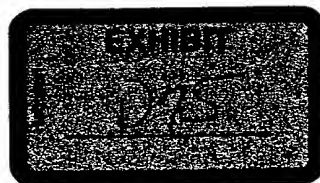
- 1) Ladder
- 2) pCRIT/gp19uads (Ferry) / Kp41
- 3) Kp41
- 4) Bam + Xba
- 5) pC1/gp19u (Ferry) / EcoRI
- 6) pCDNA3 / EcoRI
- 7) pCDNA3 / Bam + Xba.



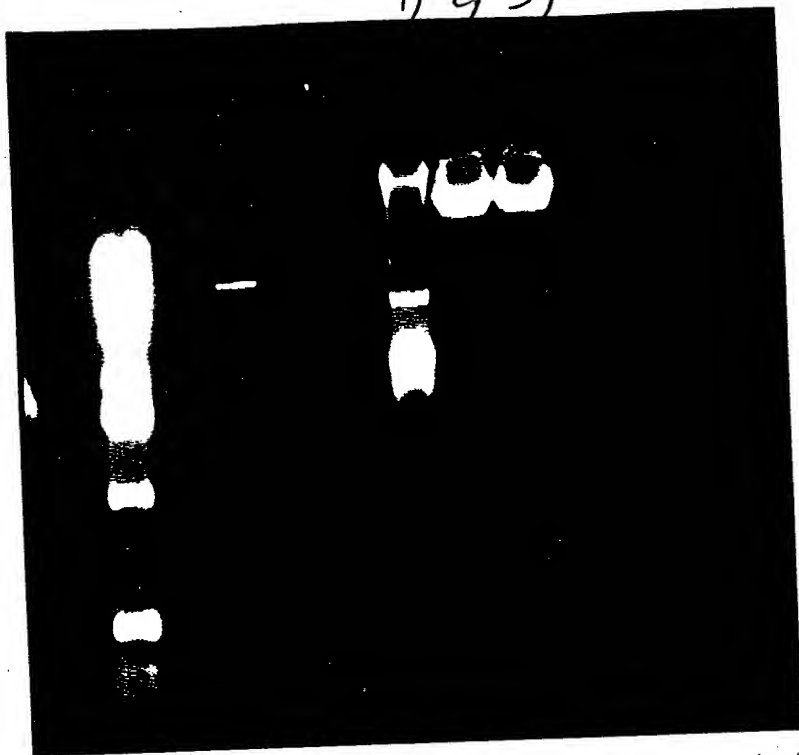
- 1) Ladder
- 2) gp19u ads Bam-Xba fr.
- 3) pCDNA3 Bam-Xba vector.

Ligation:

- 1) vector 5 μ l
- 2) vector lig 5 μ l
- 3) vector + insert
5 μ l 5 μ l



1) 2) 3)



1) colder
2) PCR / 8p194 AdS / Ben +
3) - - - - - / Ast 11071
X6e

If doesn't
look like AdS 7p194.

check with Pst1
check with Terry!

4/27

1-11/24

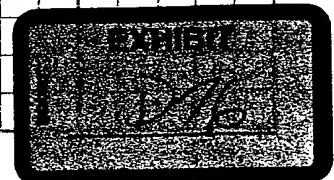


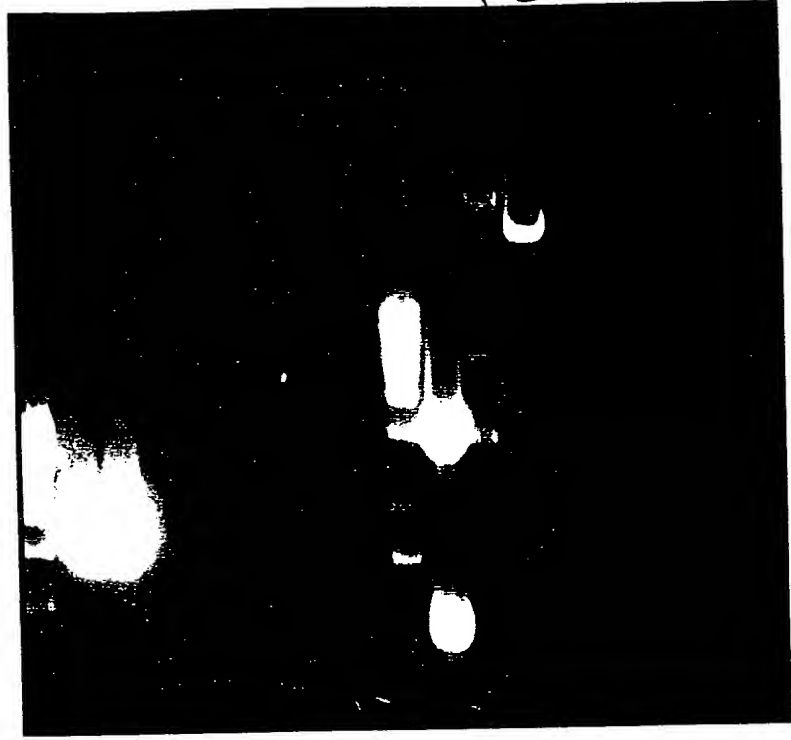
1) colder
2) PCR / 8p194 AdS / Pst

there is a small
fragment!

this is Ad2 gp is a
in reverse orientation!?

check with Van Tu.





4/28.

1) ladder.

2) pcr4 / 8p14k / HindIII

~ 500 bp fragment?

4/28.

PCR / 8p14k

restriction digestion

1) ladder

2) pcr1 / 8p14k

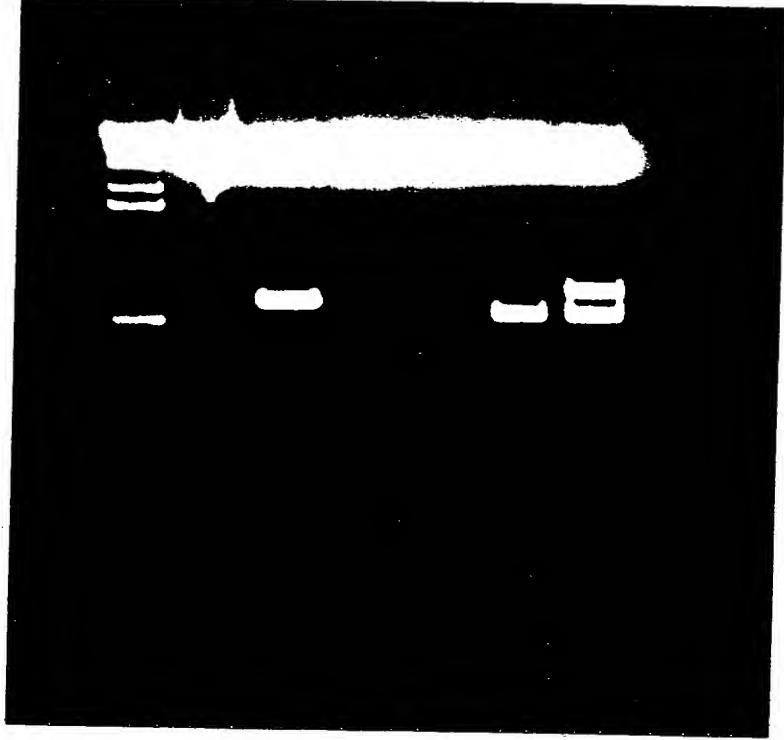
3) ——— / EcoRI

4) ——— / KpnI

5) ——— / PstI

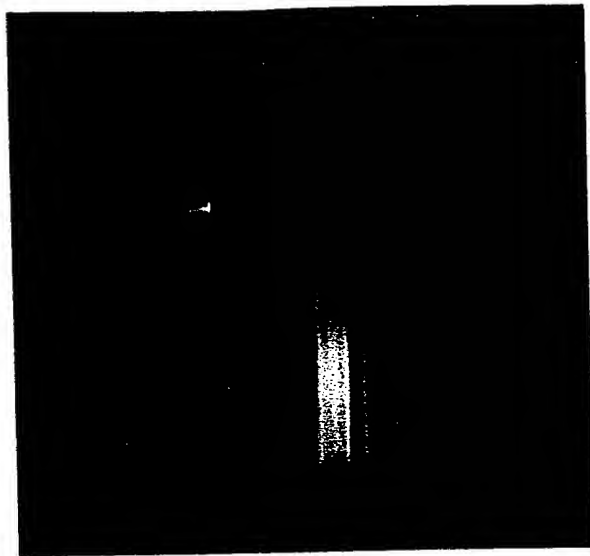
6) ——— / HindIII

7) ——— / HindIII
80mM



4/30/97

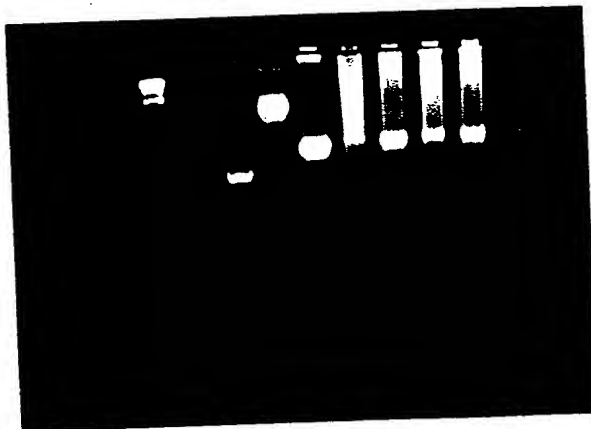
4/29/97 Restriction digestion of 111 plagues



- 1) ladder
- 2) 1101/1107 DNA
- 3) 111-1 (new) } Bam HI
- 4) 111-2 } Xba I
- 5) 111-3
- 6) 111-4

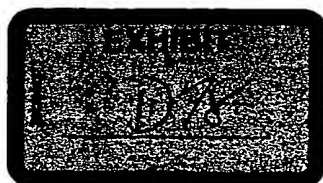
111-2, 3, 4 - look like recombinants

4/30/97
PCR analysis of
111 plagues,
primers 101, 107



- 1) ladder
- 2) blank
- 3) 114
- 4) pG114
- 5) p111
- 6) 111-1
- 7) 111-2
- 8) 111-3
- 9) 111-4

Conclusion is \Rightarrow all plagues are



4/30 Ligation:

cloning experiment 14. (14 ex).

- 1) Vector p223 / Bst 11071 + Xba I (PEB prep.)
- 2) Vector p223 / Bst 11071 + Xba I (Wikit prep.)
- 3) Insert 11011107 PCR ITR / Bst 11071 + Xba I
(without gel purification).

S/S. Comparing growth properties of: (plaque efficiency)

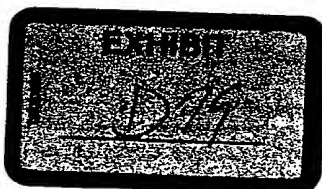
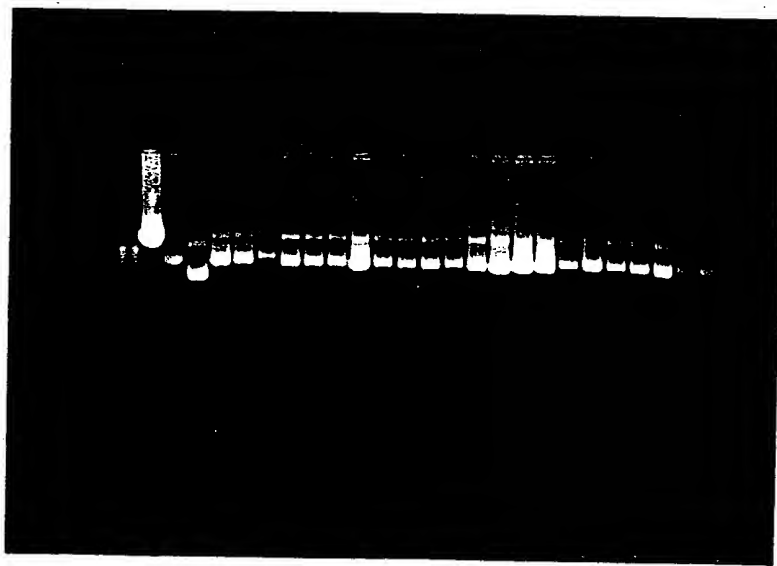
54 (4)	Controls	309
101 (1)		11011107
111 (1)		7001
111 (2)		m1 m41 (pm 734.1)

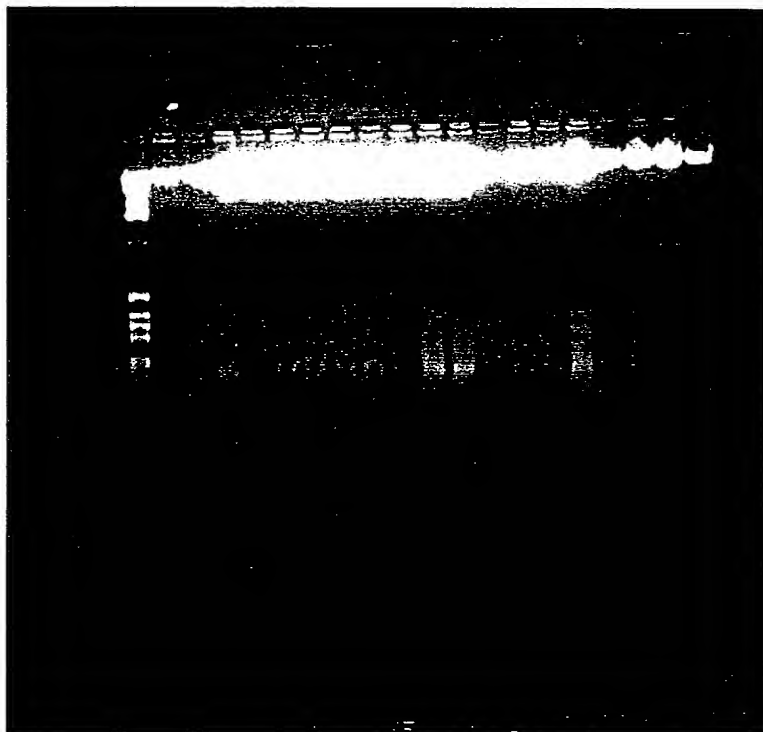
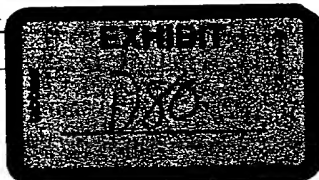
8/6/97

Minipreps of 14 ex.

- 1) ladder
- 2) p82
- 3) p223
- 4) 12ex-1
- 5)
- 6) 14ex1 (1-3)
- 7)
- 9) 14ex2 (1-20)
- 10)
- ↓
- 26)

⇒ 12ex-1 - junk.





4/6/97

1) ladder

↓ XG + Nde
restriction of
~~2~~ 14 ex clones

2) p223

↓ 141 (A3)

↓ 142 (1-20)

XG +
Nde

Clones:

141-3

142 -

- 1, 2, 3,

5, 6, 7, 8, 9, 10,

13,

15, 16, 17, 18, 19

on line

4/7/97

1) ladder

2) p223

3) 141 (3)

4) 142 (1)

5) 142 (2)

6) 142 (3)

7) 142 (5)

8) 142 (6)

9) 142 (7)

10) 142 (8)

11) 142 (9)

12) 142 (10)

13) 142 (13)

14) 142 (15)

15) 142 (16)

16) 142 (17)

17) 142 (18)

18) 142 (19)

19) 141 (11) (wt)

All rec
clones
from A
are
rec-ts.

BS 2171
(BS 11071)
+ XG L

20/142 (19)
wt)

4/8

Sequencing

- u) 25 - p141(3) - primer u) 16
- u) 26 - p141(3) - ~~u) 17~~ u) 17
- u) 27 - p142(1) - ~~u) 16~~ u) 16
- u) 28 - p142(1) - ~~u) 17~~ u) 17

sequencing
Didn't work

sequence is OK.

4/14. properly vectors pBSSK(+)/Sug 1. ucl. 30°C
p142(1) Bam + Nde. ucl

rec 700, pm 734.1 predicted
fragments length for Srf1-Nde
digestion:

19549
7981
4846
3559

Ligation:

Cloning exp 15 (p142(1) Bam + Nde + pEG1 ucl
Bam-Nde B.f.)

Cloning exp 16 (pBSSK Sug + rec 700 / Srf + Nde + T4 pol)

Cloning exp 17 (pBSSK Sug + pm 734.1 / Srf + Nde + T4 pol)

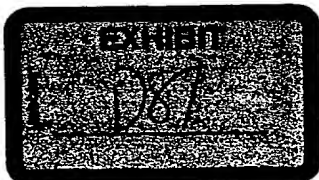
5/16 Results of transform. DMS α with 15, 16, 17 ex:

15 v - 1
15 vL - 14
15 ex - 25

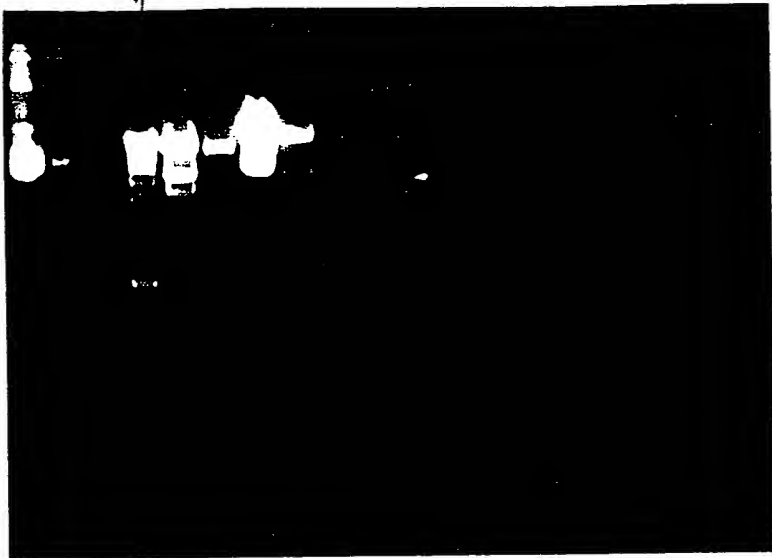
15-2 - MW as 82
others either wt 142-1 or small
plasmids

16 v - 0
16 vL - 2R + 1W
16 ex - 5R + 19W
17 ex - 7W

} all wt or same size



12 3 4



4/20

- 1) p82
- 2) p152

~~172~~ 172

1) ladder

- 2) p82 } Bonnell
- 3) p152 } Nde1

4) p82 } Nde1

5) p152 } X63

Conclusion: 152 is ok,
making cell prep.

5/25 Miniprep of 17ex

17ex - 2 (Klebs) - excise fragment from gel

1) ladder

2) p82 (+)

3) 17ex

↓

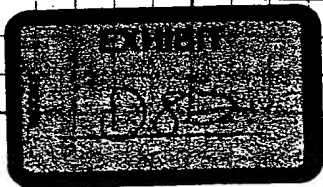
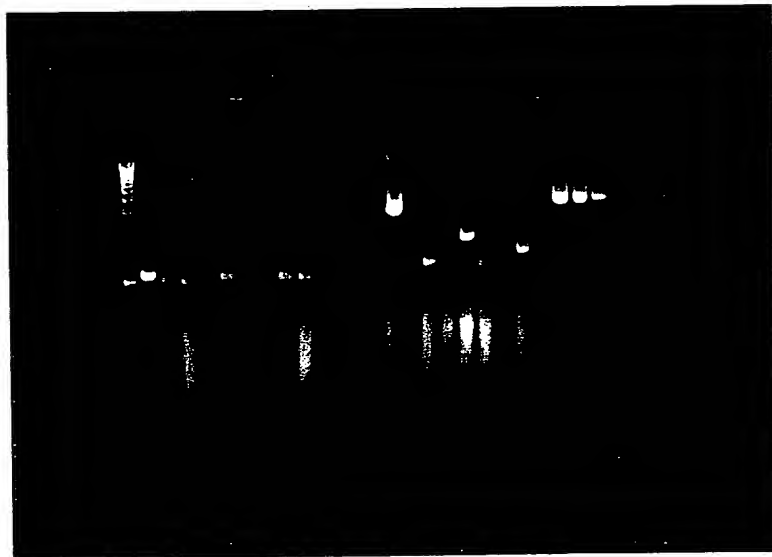
1-12

17ex2

1-12

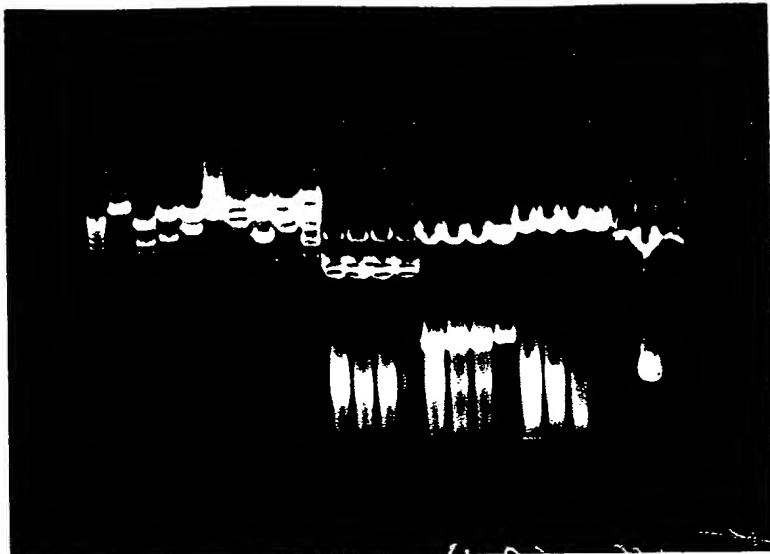
Take 172-1, 10, 11, 12

172-5? } possibly
172-8? } some junk.



5/29/97

22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



- 1) ladder
- 2) p82
- 3) p82 / Bam + Nde
- 4) p82 / Nde + Xba
- 5) p82 / bst 1107 I
- 6) p152
- 7) p152 / Bam + Nde
- 8) p152 / Nde + Xba
- 9) p152 / bst 1107 I
- 10) 734.1 (Srf + Nde)
- 11) 1721
- 12) 17210
- 13) 17211
- 14) 17212
- 15) 1721
- 16) 17210
- 17) 17211
- 18) 17212
- 19) 1721
- 20) 17210
- 21) 17211
- 22) 17212
- 23) pC19p191C / Xba + Xho
- 24) 1101/1107 / Spe + EcoRI

Conclusion: 152 is as expected.

17 ex clones have correct insert in some (direct) orientation (EcoRI digestion) Xba doesn't cut insert due to methylation of Xba site.

The insert could be cut out with BamI-SbfI to clone it into pCDNA3.1 BamI-XhoI sites.



5/28/97

Transfection 1101/1107 EcoRI + SpeI + p152.

6 dishes 293/TTC

8 dishes 293

293 TTC.

2 dishes - control. (1 ml)

2 - TTC (1 ml)

4 dishes - experiment. 2 - + conc/TTC (1 ml).

5/29/97

Cloning 18 ex:

172 BamI + SalI + XbaI (last) \Rightarrow 3.5 kb (A)
fragment. (1.1 kb) + CIP \Rightarrow (buffer)

pCDNA3.1 BamI + XhoI \Rightarrow vector
700 5.0 kb \Rightarrow (buffer)

V(9M) = 8, VL \approx 30, ex \sim 300; 1L(10M) -

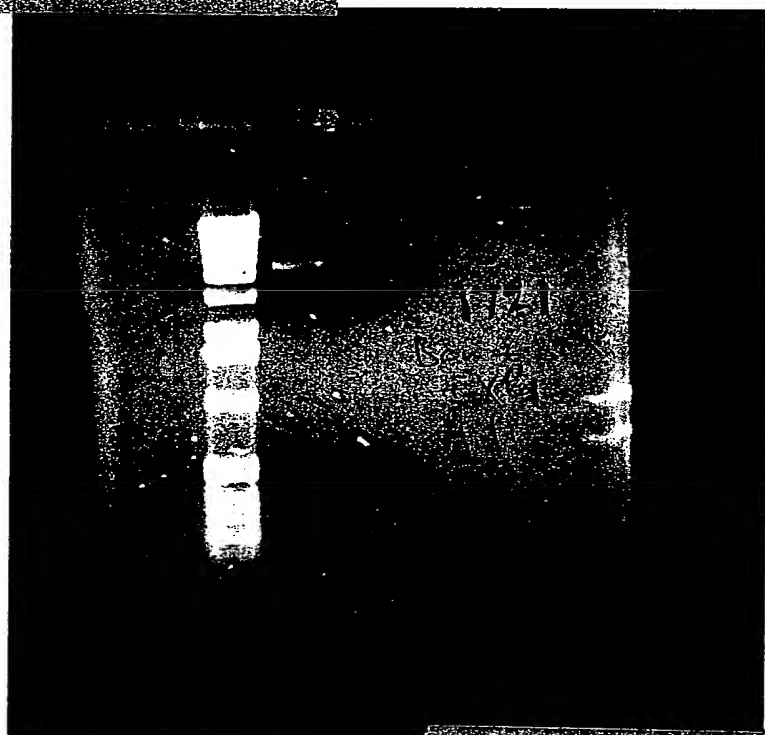


EXHIBIT
D84

First cell culture
experiment with
KO1, -2, -3
5/15/97

5/8/97 Plaque assay of E3 viruses 293 cells

Day	Number of plaques	Plaque size (mm)										
Virus (number of replicates)	3	4	5	6	7	8	9	10	11	12	13	14
309 (2)	1/1	8/2	~100/1-5	~300/1-5	~500/1-5	Same	Same	Complete CPE ~1000	Complete CPE			
110/1107 (1)	0/0	0/0	~20/1-2	~50/1-5	~100/1-5	Same	~100	~200				
(2)	0/0	0/0	~50/1-2	~20/1-5	~50/1-5	Same	~100	~300				
(1)	0/0	0/0	5/1	10/1-2	10/1-2	Same	~30	50				
7001 (3)	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0				
(2)	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0				
pm T34.1 (4)	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	~30			
(3)	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0			
(2)	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0/0	0			
544 (4)	0/0	0/0	0/0	18/1-2	20/1-5	30/1-5	~60/1-5	~100				
(3)	0/0	0/0	0/0	1/1	4/1-2	Same	0/0	30				
101-1 (4)	6/1	15/1-2	>100/1-5	>300/1-5	>1000	Same	Complete CPE	Complete CPE				
(3)	0/0	0/0	~50/1-5	~50/1-5	700	Same	>300	>300				
(2)	0/0	0/1	~15/1-5	~30/1-5	>300	Same	>20 large	100				
111-1 (4)	6/2	9/2-8	>100/1-10	>300/1-10	>1000	Same	Complete CPE ~100	Complete CPE				
(3)	0/0	1/8	~50/1-10	~80/1-10	~30	Same	~300	>300				
(2)	0/0	0/0	10/1	30/1-5	~50	Same	~50 large	>50				
111-2 (4)	0/0	8/1-5	20/1-2	50/1-5	90	Same	~100	>100				
(3)	0/0	1/1	10/1	20/1-5	30	Same	~50	>50				
(2)	0/0	0/0	0/0	7/1	12	Same	~23	28				
<div> <div>15</div> <div>16</div> <div>18</div> <div>19</div> <div>22</div> <div>23</div> <div>24</div> <div>25</div> </div>												
309 (2)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
110/1107 (1)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
7001 (3)	2	3	3	3	3	3	3	3				
(2)	0	1	3	3	3	3	3	3				
pm T34.1 (4)	50	~50	~50	~70	~70	~70	23	30				
(3)	4	7	9	10	16	23	30	30				
(2)	0	0	1	1	2	2	2	2				
544 (2)	~100	~100	~100	~100	~100	~100	~100	~100				
(2)	33	33	33	33	33	33	33	33				
101-1 (4)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
(3)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
(2)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
111-1 (4)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
(3)	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE	CCPE
(2)	50	50	50	50	50	50	50	50				
111-2 (4)	~500	~500	~500	~500	~500	~500	~500	~500				
(3)	~500	~500	~500	~500	~500	~500	~500	~500				



7/13 IEC ADP & ES plaque development on AS4.

deg = 5 6 7 8 Friday Saturday

12

(12+1)

(14)

(15)

(18)

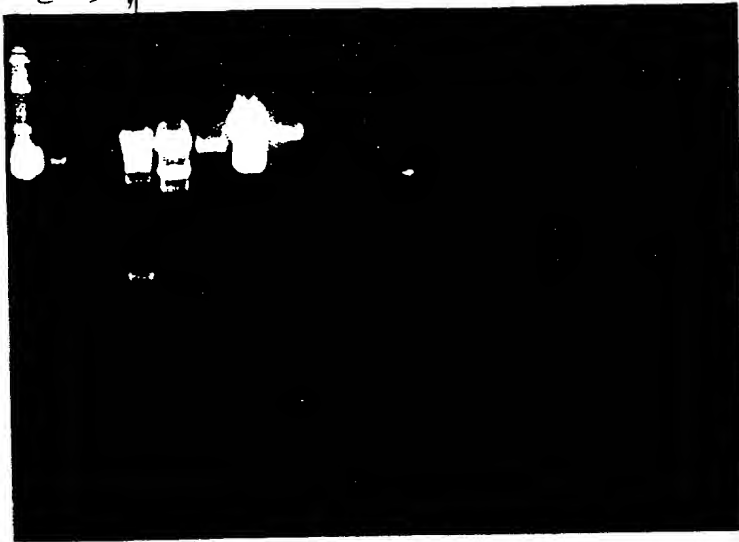
309 (~1)	12	52	~100	~100	~100	CCPE			
(~0.1+1)	1	5	14	19	20				
(~0.1-2)	3	7	19	26	27				
101/107 (~1)	0	0	3 small	8	15				
(~0.1+1)	0	0	1	3	3	5	6		
(~0.1-2)	0	0	0	0	1	2	2		
7001 (~3)	0	0	0	0	0	0	0	2	2
(~2)	0	0	0	0	0	0	0		
734.1 (~3)	0	0	0	0	0	8	8	11	15
(~2)	0	0	0	0	0	4	5	6	9
101-1 (~3)	1	11	48	60	~60				
(~2)	3?	7	20	30	34				
(~1)	0	2	3	4	7	9			
11-1 (~3)	0	6	35	50	~50				
(~2)	0	0	5	9	16				
(~1)	0	0	2	4	4				
11-2 (~4)	3?	30	70	100	~100				
(~3)	2?	4	16	20	30				
(~2)	0	0	1	4	4				
(~1)	0	0	0	0	0				



22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



12 3 4



4120

- 1) p82
- 2) p152

ladder

ladder

- 2) p82 } Bonnell
- 3) p152 } Ndel
- 4) p82 } Ndel
- 5) p152 } X62

Conclusion: 152 is all,
making cell prep.

5/25 Uniprep of 17ex

17 ex - 2 (Kleins)
- exercise fragment from gel

- 1) ladder
- 2) p65E (+)
- 3) 17ex

↓

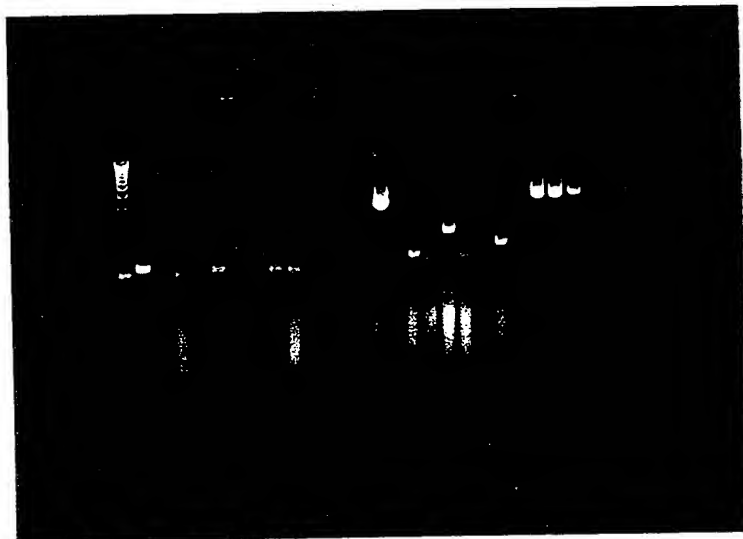
1-12

17ex2

1-12

take 72-1, 10, 11, 12

72-5? } possibly
72-8? } same sink.



EXHIBIT

D87

8944, 575/97, 5823, 97

Ray (Plagues)

virus: 5 6 7 8 9 10 11 12 13 14 15 16 17 18

303 4 12 33 45 47
8.5 25 10 15 100

#

1101/1107
7001
734.1

18 14 18 207 21
19 159 185 195 1100

12 13 11 24
50 54 70 1100

544 14 25 91 42
133 59 197 100

101-1 3 9 23 34 41
7 20 53 19 195 43/100

111-1 2 16 20 39
7 13 53 106 1100

EXHIBIT
D88

5/5/97 Player development on 295. (1. players)

Vis ^{day} 4 5 6 7 8 9 10 14 15 16 18 19 22 23 24
303 10 25 50 100 100

1101/1107 8.3 16 50 83 100

7001

~~25 50 75 100~~ ?

734.1

~~(135 235 30 33 55 76 100)~~ !

544. 3 12 27 90 100

101-1. ① 15 30 70 100

111-1 ~~20 60 100~~ ?

111-2 21 36 69 84 96 100

5/15/97 ↑ Same, 1549.

5 6 7 8 9 12 13 14

309 11 25 70 96 100

1101/1107 16 50 83 100

~~734.1~~

~~70 76 100~~ ?

101-1 18 27 36 63 82 100

111-1 25 50 100

111-2 16 66 100

EXHIBIT

D89



5/8/97 Plaque assay of E.S. viruses 293 cells

ADD

Day - Number of plaques / size (mm)

Virus (order of magnitude) (approximate)

	3	4	5	6	7	8	9	10	11
309 (~2)	1/1	8/2	~100/1-5	~300/1-5	~500/1-5	same	complete CPE	~1000	complete CPE
(~1)	0/0	0/0	~20/1-2	~50/1-3	~100/1-5	same	~100		~200
110/1107 (~2)	0/0	0/0	~50/1-2	~30/1-5	~50/1-5	same	~100		~300
(~1)	0/0	0/0	5/1	10/1-2	10/1-2	same	~30		50
7001 (~3)	0/0	0/0	0/0	0/0	0/0	0/0	0/0		2
(~2)	0/0	0/0	0/0	0/0	0/0	0/0	0/0		0
pm T34.1 (~4)	0/0	0/0	0/0	0/0	0/0	0/0	0/0		~30
(~3)	0/0	0/0	0/0	0/0	0/0	0/0	0/0		0
(~2)	0/0	0/0	0/0	0/0	0/0	0/0	0/0		0
544 (~4)	0/0	0/0	10/1	18/1-2	20/1-2	30/1-2	~60/1-2		~100
(~3)	0/0	0/0	0/0	1/1	4/1-2	same	5 (-1-2)		30
101-1 (~4)	6/1	12/1-2	>100/1-5	>300/1-5	>1000	same	complete CPE		Complete
(~3)	0/0	0/0	~50/1-5	~80/1-5	>100	same	>300		>300
(~2)	0/0	0/1	~15/1-5	~30/1-5	>30	same	>70 Range		100
111-1 (~4)	6/2	9/2-8	>100/1-10	>300/1-10	>1000	same	complete CPE ~10 ⁴		complete CPE
(~3)	0/0	1/8	~50/1-10	~80/1-10	~80	same	~300		>300
(~2)	0/0	0/0	10/1 (most 1)	30/1-5	>50	same	~50 Range		>50
111-2 (~4)	0/0	8/1-5	20/1-2	50/1-5	50	same	~100		>100
(~3)	0/0	1/1	10/1	20/1-5	30	same	~50		>50
(~2)	0/0	0/0	0/0	7/1	12	same	23		28
<div><div>15</div><div>16</div><div>18</div><div>19</div><div>22</div><div>23</div><div>24</div><div>25</div></div>									
309 (~2)	CCPE								
(~1)	CCPE								
110/1107 (~2)	30	60							
7001 (~3)	2	3	3	3	3				
(~2)	0	1	3	3	5				
pm T34.1 (~4)	~50	~60	~60	~70	~70				
(~3)	4	7	9	10	16	23	30		
(~2)	0	0	1	1	2				
544 (~4)	~100	~100	~100	~100					
(~3)	33	33	33	33					
101-1 (~4)	CCPE								
(~3)	CCPE								
(~2)	CCPE								
111-1 (~4)	CCPE								
(~3)	CCPE								
(~2)	~50	50							
111-2 (~4)	>500	~100							
(~3)	>50	~50							
(~2)	32	33							

EXHIBIT

1

D90

First cell culture experiment with
K01-2-3
5/15/97

First cell culture experiment with
K01-2,3
5/15/97

EXHIBIT

D90

5/15 Rec ADP 2 E3 plaque development on A544

deg = 5

6

7

8

Friday Saturday

12

(12+1)

(14)

(15)

(16)

CCPE

309 (~1)	12	52	~100	~100	~100	CCPE			
(~0.1+1)	1	5	14	19	20				
(~0.1-2)	3	7	19	26	27				
(~1)	0	0	3 smud	8	15				
(~0.1+1)	0	0	1	3	3	5	6		
(~0.1-2)	0	0	0	0	1	2	2		
7001 (~3)	0	0	0	0	0	0	0	2	2
(~2)	0	0	0	0	0	0	0		
734.1 (~3)	0	0	0	0	0	8	8	11	15
(~2)	0	0	0	0	0	4	5	6	9
101-1 (~3)	1	11	48	60	~60				
(~2)	3?	7	20	30	34				
(~1)	0	2	3	4	7	9			
11-1 (~3)	0	6	35	50	~50				
(~2)	0	0	5	9	16				
(~1)	0	0	2	4	4			8	11
11-2 (~4)	3?	30	70	100	~100				
(~3)	2?	4	16	20	30				
(~2)	0	0	1	4	4				7
(~1)	0	0	0	0	0				



22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

5/21/97 Plaque assay of E3 viruses on ASu9,
 (monolayer) is dying, data are not quantitative.

Plaque
 plaques

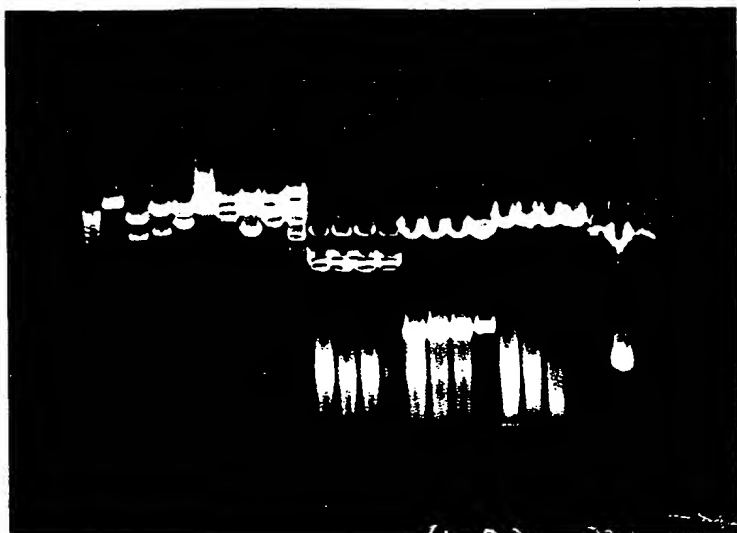
6 7 8 12 14

22-141 50 SHEETS
 22-142 100 SHEETS
 22-143 200 SHEETS



300	(~2) ~30				
	(~1) 3	12	33		
1107	(~3) 0	3	17	2.7	
	(~2) 0	3	17	3.0	
	(~1) 0	0	6	7	
00	(~4) 0	0	1	1	6
	(~3) 0	0	0	0	
734	(~4) 0	0	0		
	(~3) 0	0	0	2	3
544	(~4) 14	24	39		
	(~3) 0	0	2	3	3
	(~2) 0	0	0	0	0
101-1	(~3) 0	11	28		
	(~2) 0	3	11	12	
11-1	(~3) 0	0	3	5	
	(~2) 0	0	7	14	
11-2	(~3) 0	7	27		
	(~2) 0	0	1	2	
	(~1) 0	0		0	





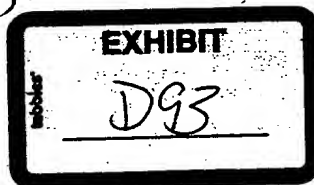
5/29/97

- 1) ladder
- 2) p82
- 3) p82 / Bam + Nde
- 4) p82 / Nde + Xba
- 5) p82 / Bst 1107 I
- 6) p152
- 7) p152 / Bam + Nde
- 8) p152 / Nde + Xba
- 9) p152 / Bst 1107 I
- 10) 734.1 / Srf + Nde
- 11) 1721
- 12) 17210
- 13) 17211
- 14) 17212
- 15) 1721
- 16) 17210
- 17) 17211
- 18) 17212
- 19) 1721
- 20) 17210
- 21) 17211
- 22) 17212
- 23) pC19p191C / Xba + Xho
- 24) 1101/1107 / Spe + EcoRI

Conclusion: 152 is as expected.

17 ex. clones have correct insert in some (direct) orientation (EcoRI digestion) Xba doesn't cut insert due to methylation of Xba site.

The insert could be cut out with BamI-SbfI to clone it into pCDNA3.1 BamI-XhoI sites.



5/28/97

Transfection 1101/1107 EcoRI + SpeI + p152.

6 dishes 293/TTF
8 dishes 293

293 TTF

2 dishes - control. (1 ml)
4 dishes - experiment. $\frac{2}{2} = \frac{\text{TTF}}{+ \text{CmV/TTF}} (1 \text{ ml})$

5/29/97

Cloning 18 ex:

172 BamI + SalI + XbaI (last) \Rightarrow 3.5 kb (A)
fragment (1 cut) + CIP \Rightarrow (buffer)

pCDNA3.1 BamI + XhoI \Rightarrow vector
700 50 kb \Rightarrow (buffer)

V(9N) - 2, VL \approx 30, ex \approx 300, LL (10 μ l) - 0

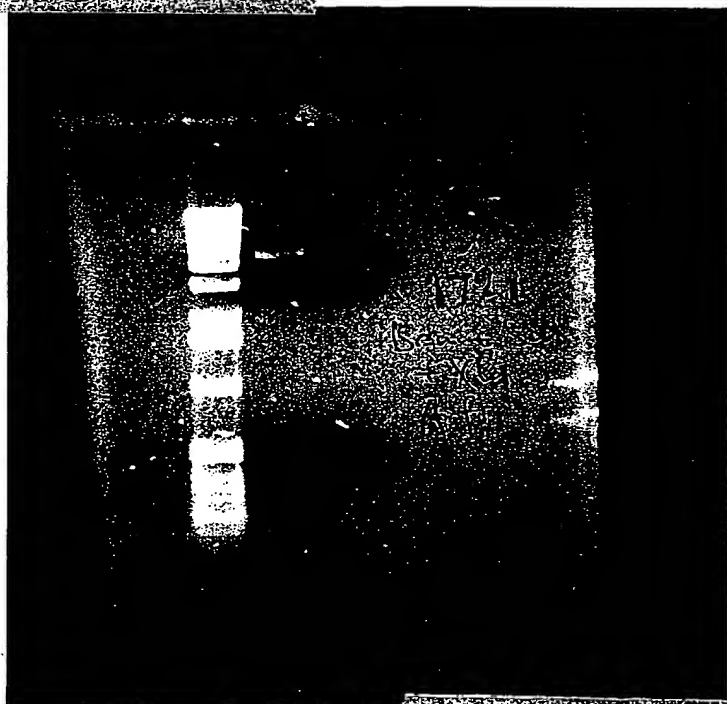


EXHIBIT
Dex

6/5/99

18 ex miniprep \Rightarrow 1-8, 10, 11 - look like
rect's
(~~green~~ MW)

1) Ladder

2) \downarrow 18 ex (1-12)

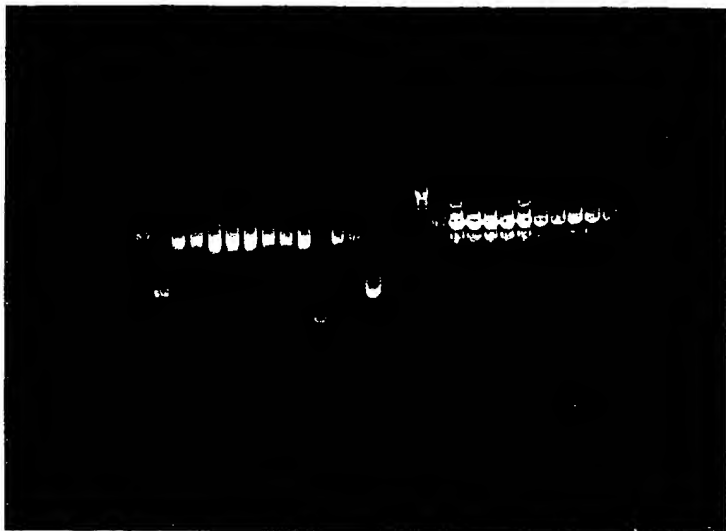
Take 1-8, 10, 11.

1) Ladder

2) pCONA3.1200(+) } Bam
3) \downarrow 18 ex } Xba
 \downarrow 1-8, 10, 11

Look like rect's.

Grow 18(1).



22-141 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS



EXHIBIT

D95

6/5/97

VIPA - Infections:

Rock, ~~1101/1107~~, 1101/1107, 544, 101-1, 111-1, 734.1,

E - early (9-15)

L - late (24-28)

(295)E	(293-1)E	(A549)	(295)	(29)TR	(A529)
M - 1	7	13	19	26	36
1101/1107 - 2	8	14	20	27	37
544 - 3	9	15	21	28	38
101-1 - 4	10	16	22	29	39
111-1 - 5	11	17	23	30	40
734.1 - 6	12	18	24	31	41

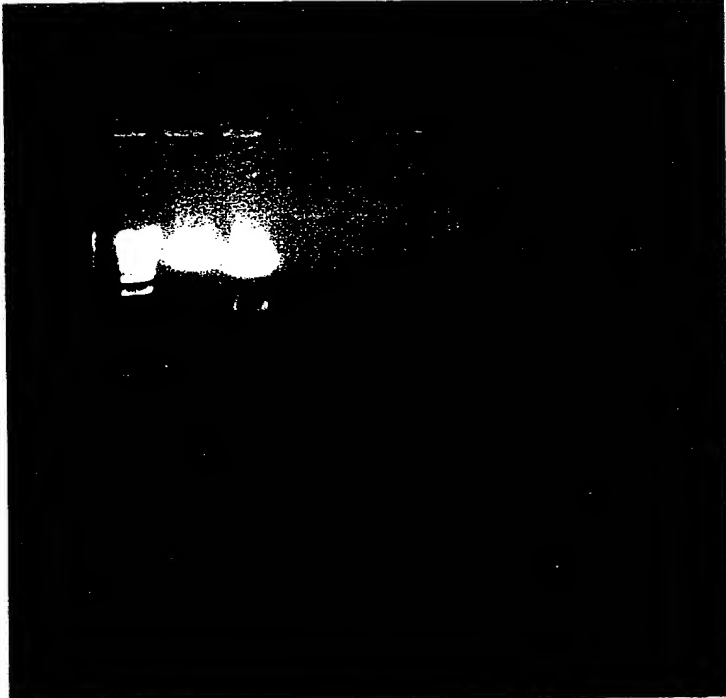
A549

1101/1107 - 100μl
 544 - 100μl
 101 - 1 - 100μl
 111 - 2 - 150μl
 734.1 - 100μl

293

1101/1107 - 100μl
 544 - 100μl
 101 - 1 - 100μl
 111 - 2 - 150μl
 734.1 - 100μl

- Viruses dosage.
 (code stocks
 of viruses)



6/10/97
 Restriction pattern
 for 181 maxiprep.

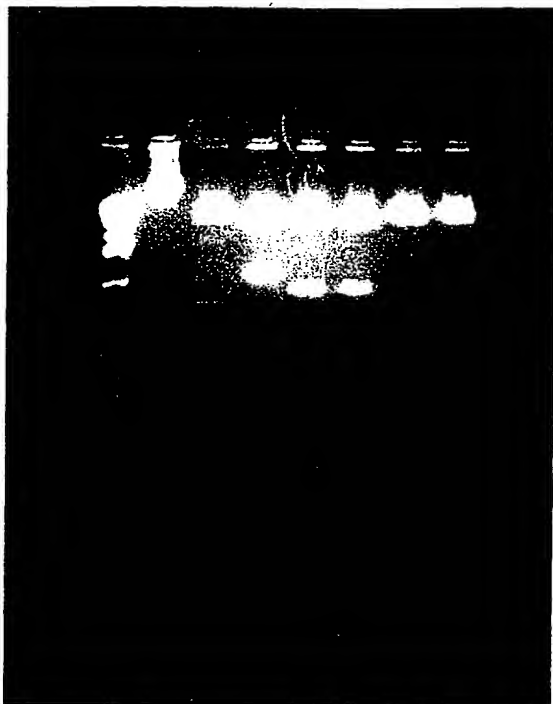
- 1) Cadder
- 2) 181/SpeI + PstI
- 3) 181/SpeI + XhoI.

Pattern is as
 expected.

EXHIBIT
 D96

6/25/97

Restriction digestion of pCI-14.7 (Terry).



1) ladder

2) pCI-14.7

3) — EcoRI

4) — BglII

5) — SpeI + XhoI

6) — SpeI + Salt

7) — BamHI + XhoI

8) — BamHI + Salt

7/1/97 Clonings 19ex; 20 ex.

19ex — vector p#30 (SmaBI); insert 19ex1 { p181, mfe, XbaI, Klenow

19ex2 { p181, mfe, RV, Klenow

20ex — vector pL2/PacI + T4; insert 20ex1 p181, MX KL

7/3 transformation M52.

20V ~10

20V ~50

20ex1 ~100

20ex11 ~30

13V ~20

19V ~100

19ex1 ~100

19ex11 ~100.

20ex2 p181

M RV KL

EXHIBIT

D97

DK



Dear Dan:

Attached is a list of primers that were ordered by Konstantin Doronin. The primers were named KD1, KD2, KD3, KD4, KD5, etc. (see Description/Sequences). These primers were used in studies on the ADP-overexpressing vectors, either for DNA sequencing or for amplification of certain sequences by the polymerase chain reaction (PCR). Also attached are Dr. Doronin's handwritten notes indicating the use of the primers. (These notes are not dated, but this list was begun when the primers were ordered). Please note that the primers were ordered on 9/26/96, 11/04/96, and 03/24/97.

Also included are some actual DNA sequence data using some of these primers to sequence some of the plasmids that were used to construct the ADP-overexpressing vectors. The dates of the sequencing runs are on the datasheets. Note that the first sequencing run was on November 19, 1996. Other runs were on November 25/26, 1996, March 20/21, 1997, April 21, 1997, May 12, 1997, and March 23/24, 1999.

Thanks,

Bill

Order Number		
Please refer to this No. on all Inquires	Order Date	Page No.
473935 A	09/26/98	1 of 1

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ST LOUIS, MO 63104
DORONIN
000127762

MLR	5903851		FAX/DEBBIE HUMISTON
-----	---------	--	---------------------

1.0	10336-022	KD1 \ DORONIN	1 Each	(G07)	19.3
	A3884G07	CTACGAGAGAACCTCTCCGAG			
2.0	10336-022	KD2 \ DORONIN	1 Each	(G08)	15.5
	A3884G08	GCCACAACCTTATACTGTTTGC			
3.0	10336-022	KD3 \ DORONIN	1 Each	(G09)	28.6
	A3884G09	TCAGCCCACGGTACTTAATTAACCCAAAAGGTGGAT			
4.0	10336-022	KD4 \ DORONIN	1 Each	(G10)	18.8
	A3884G10	GCTCTAGAAGTCAGGCTTCCTGG			
5.0	10336-022	KD5 \ DORONIN	1 Each	(G11)	17.9
	A3884G11	GCTCTAGATCTCATTTAATCATA			
6.0	10336-022	KD6 \ DORONIN	1 Each	(G12)	21.5
	A3884G12	CCTTAATTAAAAGTCAGGCTTCCTGG			
7.0	10336-022	KD7 \ DORONIN	1 Each	(H01)	20.3
	A3884H01	CCTTAATTAATCTCATTTAATCATA			
8.0	10336-022	KD8 \ DORONIN	1 Each	(H02)	21.7
	A3884H02	CGCCTATACAGAAGATTTTCCAG			
9.0	10336-022	KD9 \ DORONIN	1 Each	(H03)	20.5
	A3884H03	CGCCTATACACTGCAGCAGGTGTG			



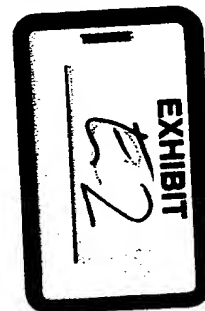
GIBCO BRL Custom Primers
Certificate of Analysis

ST LOUIS UNIV SCHOOL OF
Order Number: 473935A
Order Date: 09/26/96

Primer 1:

Primer Name: KD1
Researcher: DORONIN
Sequence (5' to 3'): CTA CGA GAG AAC CTC TCC GAG
Molecular Weight $\mu\text{g}/\mu\text{mole}$: 6740.2
Millimolar Extinction Coefficient: 230.5
Purity Deprotected
Tm (1 M Na+) 73
Tm (50 mM Na+) 51
% GC 57

Primer Number: A3884G07 (G07)
Primer Length: 21
 μg per OD: 29.2
nmoles per OD: 4.3
OD's 19.3
 $\mu\text{g's}^*$ 566
nmoles 84
Coupling Eff. 99%



Notes:

Primer 2:

Primer Name: KD2
Researcher: DORONIN
Sequence (5' to 3'): GCC ACA ACT TAT ACT GTT TGC
Molecular Weight $\mu\text{g}/\mu\text{mole}$: 6696.2
Millimolar Extinction Coefficient: 221.4
Purity Deprotected
Tm (1 M Na+) 67
Tm (50 mM Na+) 45
% GC 42

Primer Number: A3884G08 (G08)
Primer Length: 21
 μg per OD: 30.2
nmoles per OD: 4.5
OD's 15.5
 $\mu\text{g's}^*$ 471
nmoles 70
Coupling Eff. 99%

Notes:

Primer 3:

Primer Name: KD3
Researcher: DORONIN
Sequence (5' to 3'): TCA GCC CAC GGT ACT TAA TTA ACC CAA AAG GTG
GAT
Molecular Weight $\mu\text{g}/\mu\text{mole}$: 11632.2
Millimolar Extinction Coefficient: 407.2
Purity Deprotected
Tm (1 M Na+) 81
Tm (50 mM Na+) 59
% GC 44

Primer Number: A3884G09 (G09)
Primer Length: 36
 μg per OD: 28.5
nmoles per OD: 2.4
OD's 28.6
 $\mu\text{g's}^*$ 817
nmoles 70
Coupling Eff. 99%

Notes:

* -See Note about Quantities in Supporting Information.

GIBCO BRL Custom Primers Certificate of Analysis

ST LOUIS UNIV SCHOOL OF

Order Number: 473935A

Order Date: 09/26/96

Primer 4:

Primer Name: KD4

Researcher: DORONIN

Sequence (5' to 3'): GCT CTA GAA GTC AGG CTT CCT GG

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7429.6

Millimolar Extinction Coefficient: 244.0

Purity Deprotected

Tm (1 M Na+) 75

Tm (50 mM Na+) 54

% GC 56

Notes:

Primer Number: A3884G10 (G10)

Primer Length: 23

 μg per OD: 30.4

nmoles per OD: 4.1

OD's 18.6

 $\mu\text{g's}^*$ 568

nmoles 76

Coupling Eff. 99%

Primer 5:

Primer Name: KD5

Researcher: DORONIN

Sequence (5' to 3'): GCT CTA GAT CTC ATT TAA TCA TA

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7346.6

Millimolar Extinction Coefficient: 251.4

Purity Deprotected

Tm (1 M Na+) 65

Tm (50 mM Na+) 43

% GC 30

Notes:

Primer Number: A3884G11 (G11)

Primer Length: 23

 μg per OD: 29.2

nmoles per OD: 3.9

OD's 17.9

 $\mu\text{g's}^*$ 523

nmoles 71

Coupling Eff. 99%

Primer 6:

Primer Name: KD6

Researcher: DORONIN

Sequence (5' to 3'): CCT TAA TTA AAA GTC AGG CTT CCT GG

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 8370.2

Millimolar Extinction Coefficient: 284.9

Purity Deprotected

Tm (1 M Na+) 73

Tm (50 mM Na+) 51

% GC 42

Notes:

Primer Number: A3884G12 (G12)

Primer Length: 26

 μg per OD: 29.3

nmoles per OD: 3.5

OD's 21.5

 $\mu\text{g's}^*$ 634

nmoles 76

Coupling Eff. 99%

* - See Note about Quantities in
Supporting Information.



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GIBCO BRL Custom Primers
Certificate of Analysis**ST LOUIS UNIV SCHOOL OF****Order Number: 473935A****Order Date: 09/26/96****Primer 7:**

Primer Name: KD7

Researcher: DORONIN

Sequence (5' to 3'): CCT TAA TTA ATC TCA TTT AAT CAT A

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7957.0

Millimolar Extinction Coefficient: 277.0

Purity Deprotected

Tm (1 M Na+) 63

Tm (50 mM Na+) 41

% GC 20

Notes:

Primer Number: A3884H01 (H01)

Primer Length: 25

 μg per OD: 28.7

nmoles per OD: 3.6

OD's 20.3

 $\mu\text{g's}^*$ 585

nmoles 73

Coupling Eff. 99%

Primer 8:

Primer Name: KD8

Researcher: DORONIN

Sequence (5' to 3'): CGC GTA TAC AGA AGA TTT TTC CAG

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7742.8

Millimolar Extinction Coefficient: 268.2

Purity Deprotected

Tm (1 M Na+) 70

Tm (50 mM Na+) 49

% GC 41

Notes:

Primer Number: A3884H02 (H02)

Primer Length: 24

 μg per OD: 28.8

nmoles per OD: 3.7

OD's 21.7

 $\mu\text{g's}^*$ 628

nmoles 81

Coupling Eff. 99%

Primer 9:

Primer Name: KD9

Researcher: DORONIN

Sequence (5' to 3'): CGC GTA TAC ACT GCA GCA GGT GTG

Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7784.8

Millimolar Extinction Coefficient: 281.8

Purity Deprotected

Tm (1 M Na+) 77

Tm (50 mM Na+) 56

% GC 58

Notes:

Primer Number: A3884H03 (H03)

Primer Length: 24

 μg per OD: 29.7

nmoles per OD: 3.8

OD's 20.5

 $\mu\text{g's}^*$ 609

nmoles 78

Coupling Eff. 99%

* -See Note about Quantities in
Supporting Information.LIFE  TECHNOLOGIES™

Order Number		
Please refer to this No. on all Inquires	Order Date	Page No.
522393 A	11/04/96	1 of 1

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000127752

PERSONNEL NO.	CUSTOMER P.O. NO.	CUSTOMER PHONE/FAX/STREET ADDRESS	IN AGENCY
CEH	SB03851		FAX/DEBBIE HUMISTON

1.0	10336-022	KD 10 \ DORANIN	1 Each	(B02)	12.6
	A4379B02	ACACGGCACCAGCTCAATCAG			
2.0	10336-022	KD 11 \ DORANIN	1 Each	(B03)	12.5
	A4379B03	CGGAGTAACTTGTATGTGTTG			



GIBCO BRL Custom Primers
Certificate of Analysis**ST LOUIS UNIV SCHOOL OF****Order Number: 522393A****Order Date: 11/04/96****Primer 1:**

Primer Name: KD 10
Researcher: DORANIN
Sequence (5' to 3'): ACA CGG CAC CAG CTC AAT CAG
Molecular Weight $\mu\text{g}/\mu\text{mole}$: 6709.2
Millimolar Extinction Coefficient: 232.1
Purity **Deprotected**
Tm (1 M Na+) 73
Tm (50 mM Na+) 51
% GC 57

Notes:

Primer Number: A4379B02 (B02)
Primer Length: 21
 μg per OD: 28.9
nmoles per OD: 4.3
OD's 12.6
 $\mu\text{g's}^*$ 366
nmoles 54
Coupling Eff. 98%

Primer 2:

Primer Name: KD 11
Researcher: DORANIN
Sequence (5' to 3'): CGG AGT AAC TTG TAT GTG TTG
Molecular Weight $\mu\text{g}/\mu\text{mole}$: 6847.2
Millimolar Extinction Coefficient: 233.0
Purity **Deprotected**
Tm (1 M Na+) 67
Tm (50 mM Na+) 45
% GC 42

Notes:

Primer Number: A4379B03 (B03)
Primer Length: 21
 μg per OD: 29.3
nmoles per OD: 4.2
OD's 12.5
 $\mu\text{g's}^*$ 369
nmoles 53
Coupling Eff. 98%

* -See Note about Quantities in
Supporting Information.

**LIFE TECHNOLOGIES™**

Order Number		
Please refer to this No. on all Inquires	Order Date	Page No.
409887 A	03/24/97	1 of 1

SOLD TO

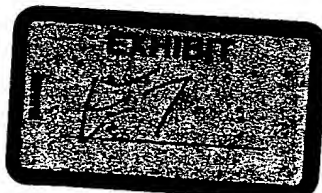
ST LOUIS UNIV
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1402 S GRAND BLVD
MOLEC MICRO/RM M410
ST LOUIS, MO 63104
DEBBIE HUMISTON
000127752

CD	SHIP TO	SHIP TO	SHIP TO
	S903850		DEBBIE HUMISTON

1.0	10336-022	KD12 \ DORONIN	1 Each	(D10)	16.4
	A6280D10	CCTTAATTAATCTAGAGATCTTATCCCTTT			
2.0	10336-022	KD14 \ DORONIN	1 Each	(D11)	14.7
	A6280D11	GGGGTACGAAGCCATCTGCAACAACAT			
3.0	10338-022	DK15 \ DORONIN	1 Each	(D12)	13.7
	A6280D12	CCTTAATTAATCTAGAGTCAGTTAGCCTCCCC			
4.0	10336-022	KD16 \ DORONIN	1 Each	(E01)	14.6
	A6280E01	CGCGCGTATACACTTCCCATTTTAAG			
5.0	10336-022	KD17 \ DORONIN	1 Each	(E02)	12.9
	A6280E02	GCTCTAGACATCATCAATAATAT			



GIBCO BRL Custom Primers
Certificate of Analysis**ST LOUIS UNIV SCHOOL OF****Order Number: 409867A****Order Date: 03/24/97****Primer 4:****Primer Name: KD18****Researcher: DORONIN****Sequence (5' to 3'): CGC GCG TAT ACA CTT CCC ATT TTA AG****Molecular Weight $\mu\text{g}/\mu\text{mole}$: 8306.2****Millimolar Extinction Coefficient: 272.6****Purity Deprotected****Tm (1 M Na+) 74****Tm (50 mM Na+) 53****% GC 46****Notes:****Primer Number: A6280E01 (E01)****Primer Length: 28** **μg per OD: 30.4****nmoles per OD: 3.6****OD's 14.5** **$\mu\text{g's}^*$ 444****nmoles 53****Coupling Eff. 99%****Primer 5:****Primer Name: KD17****Researcher: DORONIN****Sequence (5' to 3'): GCT CTA GAC ATC ATC AAT AAT AT****Molecular Weight $\mu\text{g}/\mu\text{mole}$: 7364.6****Millimolar Extinction Coefficient: 263.4****Purity Deprotected****Tm (1 M Na+) 66****Tm (50 mM Na+) 43****% GC 30****Notes:****Primer Number: A6280E02 (E02)****Primer Length: 23** **μg per OD: 27.9****nmoles per OD: 3.8****OD's 12.9** **$\mu\text{g's}^*$ 361****nmoles 49****Coupling Eff. 99%*** -See Note about Quantities in
Supporting Information.**LIFE TECHNOLOGIES.**

Primers:

1) KD1 - CTA'CGA'GAG'AAC'CTC'TCC'GAG'

Comment - primer from Ad5 sequence ~ 50 nt left from ~~Start~~ site -
for PCR mutation of gp13K (E3) - Left primer.

2) KD2 - GCC'ACA'ACT'TAT'ACT'GTT'TCC

Comment - primer from Ad5 sequence ~ 50 nt right from Bst 1107I site
- for PCR mutation of gp13K (E3) - right primer.

3) KD3 - TCA'GCC'CAC'GGT'ACT'TAA'TTAA'CC'CAA'AAG'GTG'GA

Comment - middle primer for mutation of gp13K E3 protein gene.
inserting PacI site with TAA stop codon to the ORF
destroying KpnI site simultaneously, to be used 1 with KD2,
then product used as primer with KD1.

4) KD4 - GC'TCT'AGA'AGT'CAG'GCT'TCC'TGG

Comment - left primer for PCR of 11.6K E3 with XbaI site.

5) KD5 - GC'TCT'AGA'TCT'CAT'TTA'ATC'ATA

Comment - right primer for PCR of 11.6K E3 with XbaI site.

6) KD6 - CC'TTAATTAA'GT'CAG'GCT'TCC'TGG

Comment - left primer for PCR of 11.6K E3 with PacI site

7) KD7 - CC'TTAATTAA'TCT'CAT'TTA'ATC'ATA

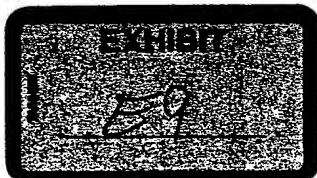
Comment - right primer for PCR of 11.6K E3 with PacI site.

8) KD8) CGC'GTATAC'AGA'AGA'TTTTTC'CAG'

upstream primer with Bst 1107I site for PCR of SP-B 500 promoter.

9) KD9) CGC'GTATAC'ACT'GCA'GCA'GGT'GTC

downstream primer with Bst 1107I site for PCR of SP-B 500 promoter.

22-143 50 SHEETS
22-142 100 SHEETS
22-144 200 SHEETS

Primers for sequencing ϕ EV substitutions ;
promoter.

- 10) K1 (10): ACA' CCG' CAC' CAG' CTC' AAT' CAG' (left)
11) K1 (11): CCG' AGT' AAC' TTG' TAT' GTG' TTG' (right)

Primers for TK insert into Pac and Xba sites. (double PCR,
12+14, then product with 15
on Ad template).

CC
~~CCG~~ TTAATTAA TCTAGA GAT' CTT' ATT' CCC' TTT

Primer with PacI and XbaI sites + Ad seq 30818 \rightarrow
upstream primer.

14) K1 (14) \leftarrow ortho.

GGG' GTA' CGA' AGC' CAT' CTG' CAA' CAA' CAT'

Primer left half from 5' tkorf, right half - from Ad ~ 31080 \rightarrow
 \Rightarrow beginning of fiber gene. to prevent methylation.

K1 (15)
15) ~~CC~~ TTAATTAA TCTAGA G TCA' GTT' AGC' CTC' CCC
ortho tkorf.

Primers to PCR Ad5 right ITR (Ad. 35773-35935) with
flanking bst1107I and XbaI sites. respectively.

K1 (16)
16) CCGGC GTATAC ACTTCC' CAT' TTT' AAG

K1 (17)
17) GC TCTAGA CAT' CAT' CAA' TAA' TAT

K1 (18) - Direct - GTA - GAG - TTT - TCT - CCT - CCG
for PCR and sequence of 1101/1107 dl.

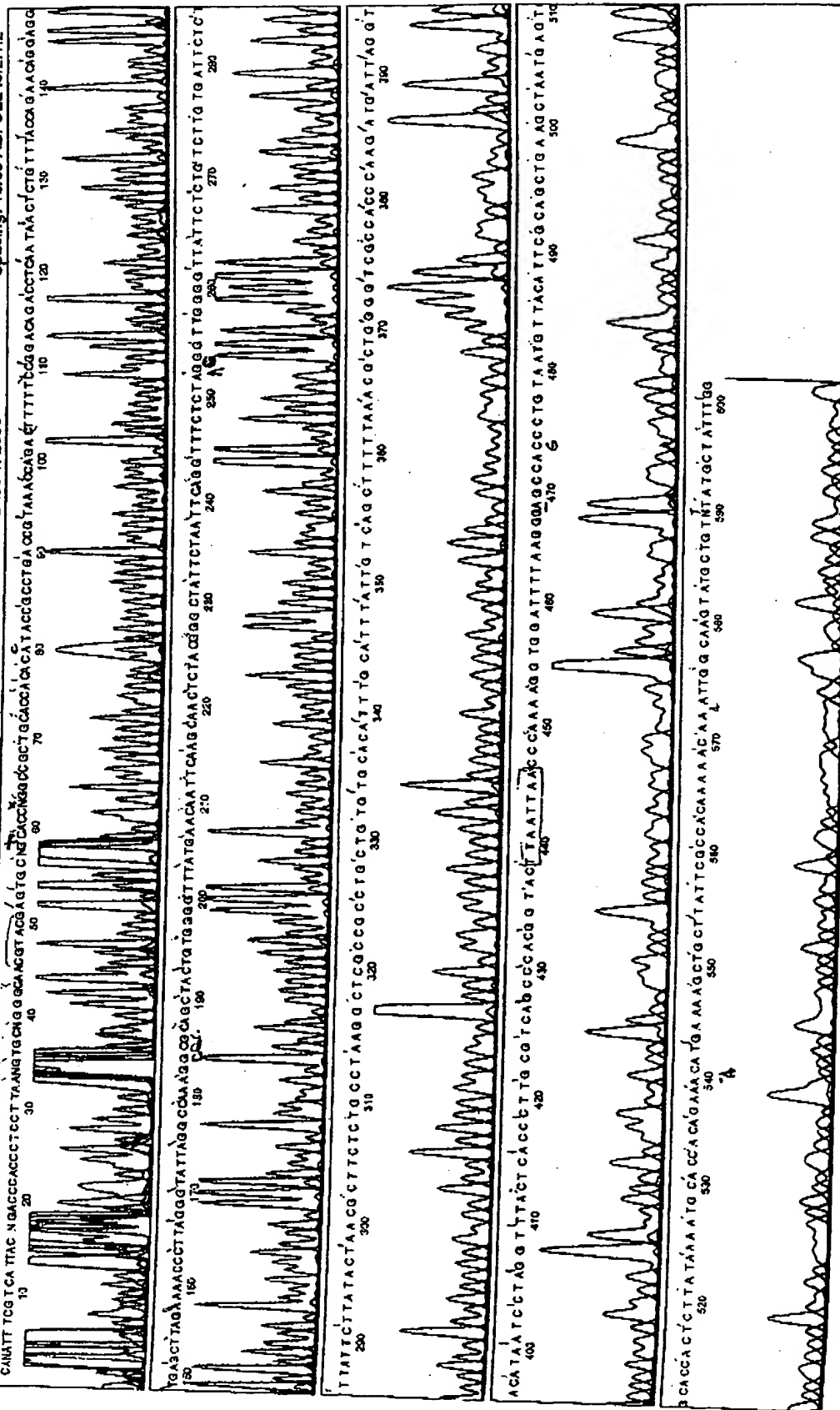
K1 (19) - Reverse - CCC - TCT - TCA - TCC - TCG - TCG

K1 20 - TCT, ACT, TTA, ACC, CCA, TCT, CCG C E3 direct to C1 d1)

K1 21 - CCG, AGG, TGT, TAT, TAC, CGA, AGA C E1A direct to M01 d1)

K1 22 - TGA, CCG, AAC, CCG, TAA, AGT, CCA (from E4 prom d1)
direct

30X clone 1
Model 310
Version 2.12
ABI PRISM
A1-KD primer 1 (2) L
KD
Lane 1
Signal G:340 A:481 T:305 C:253
DT POP6 10-10-96
POP6DT.Matrx
Points 2080 to 10200 Base 1: 2080
Page 1 of 1
Nov 19, 1996 2:40 PM
Nov 19, 1996 11:42 AM
Spacing: 13.83 ABI-CE2 for 2.1.2



Signal G:182 A:289 T:155 C:92
DT POP6 10-10-98
POP6DT Matrix
Points 2050 to 11480 Base 1: 2050

Nov 26, 1996 9:53 AM
Nov 25, 1996 7:38 PM
Spacing: 12.80 ABI-CE2 for 2.1.2

Model 910
Version 2.1.2

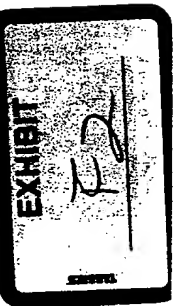
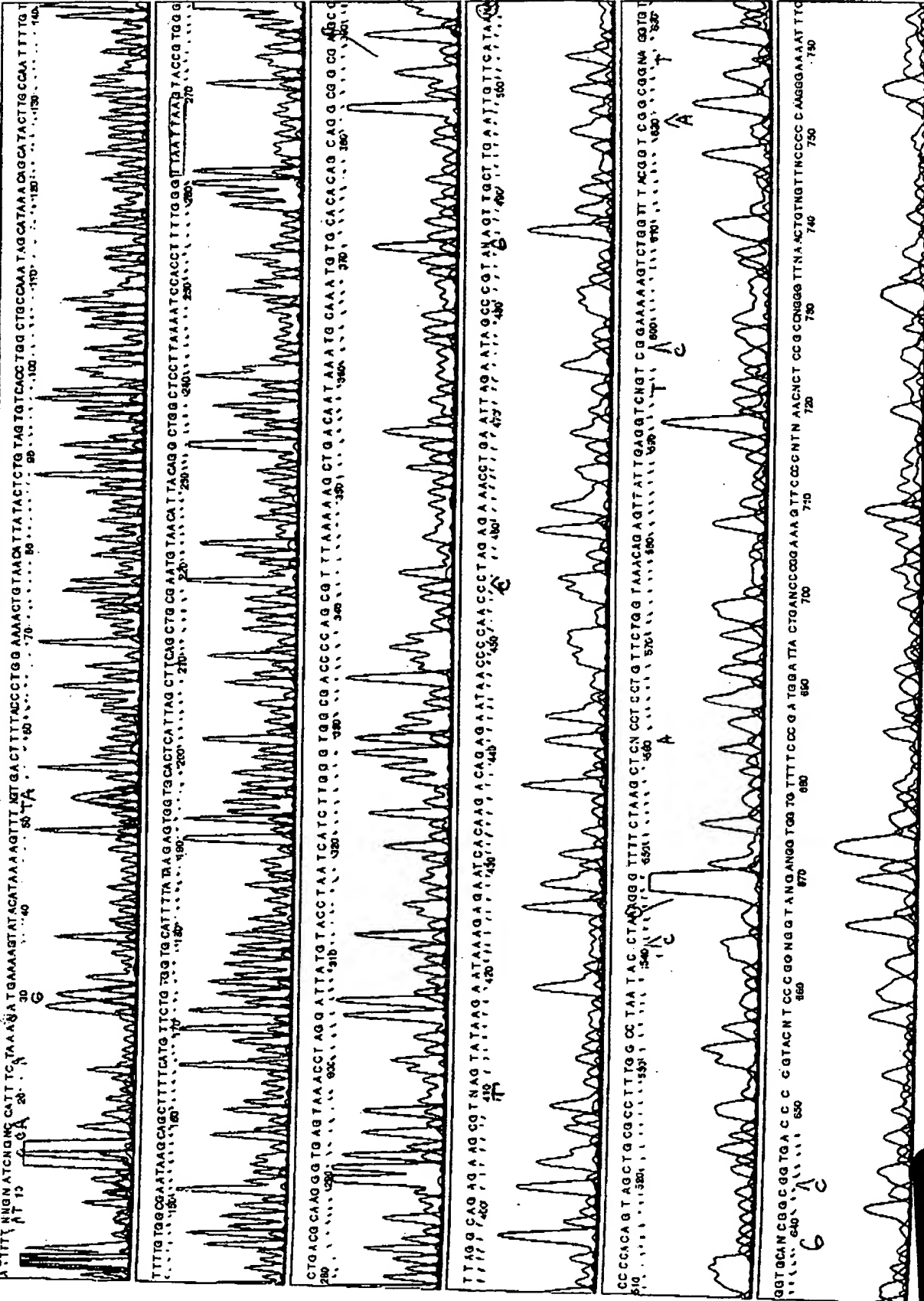


A5-KD-#2

KD-#2

Lane 3

3 ex done 1
minor 132



[illegible]

EXHIBIT

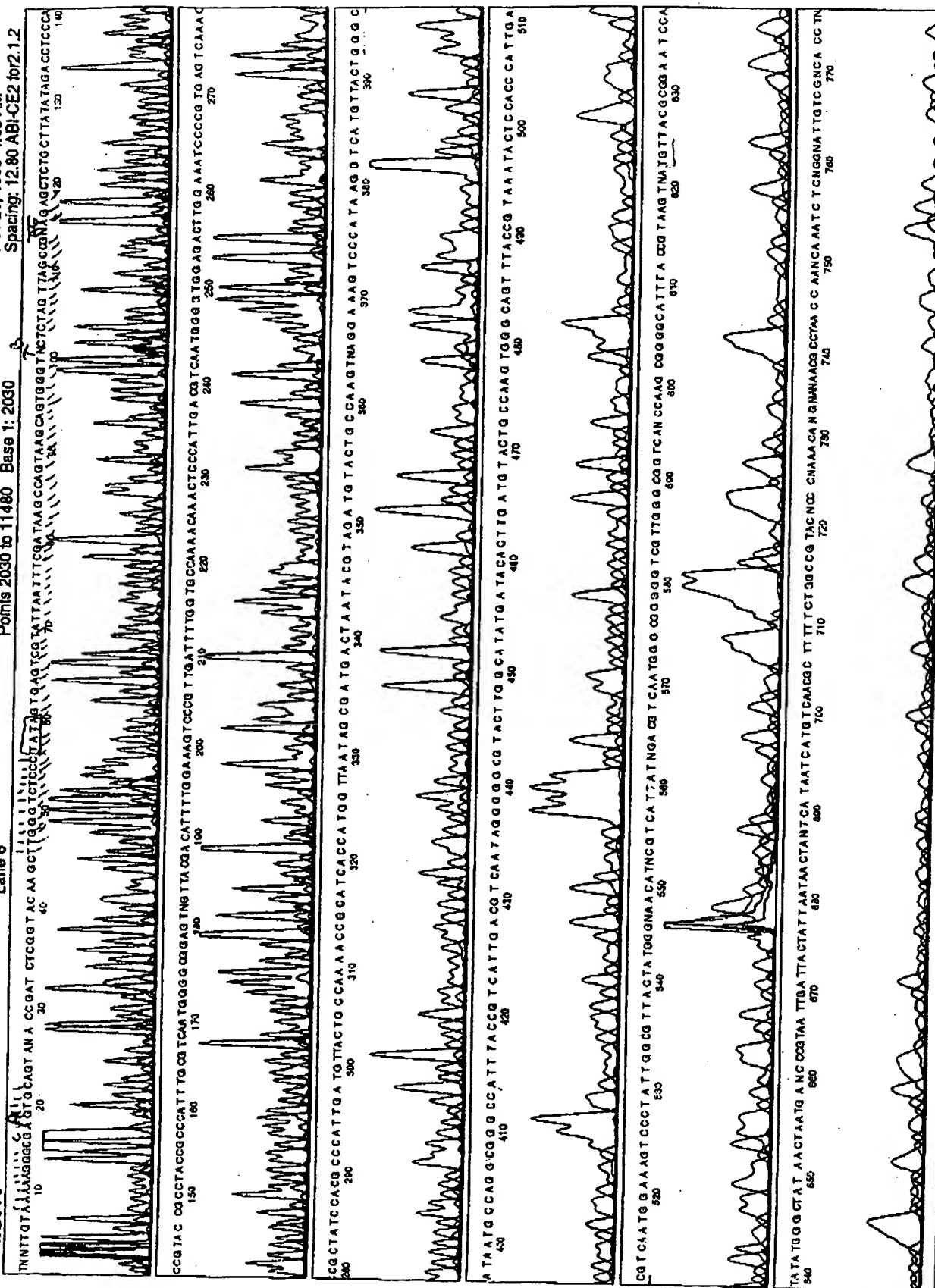
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SEARCHED

Spacing: 12.86 ABI-CE2 to 2.1.2



Spacing: 12.80 ABI-CE2 to 2.1.2

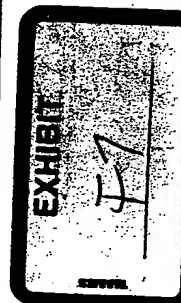


15

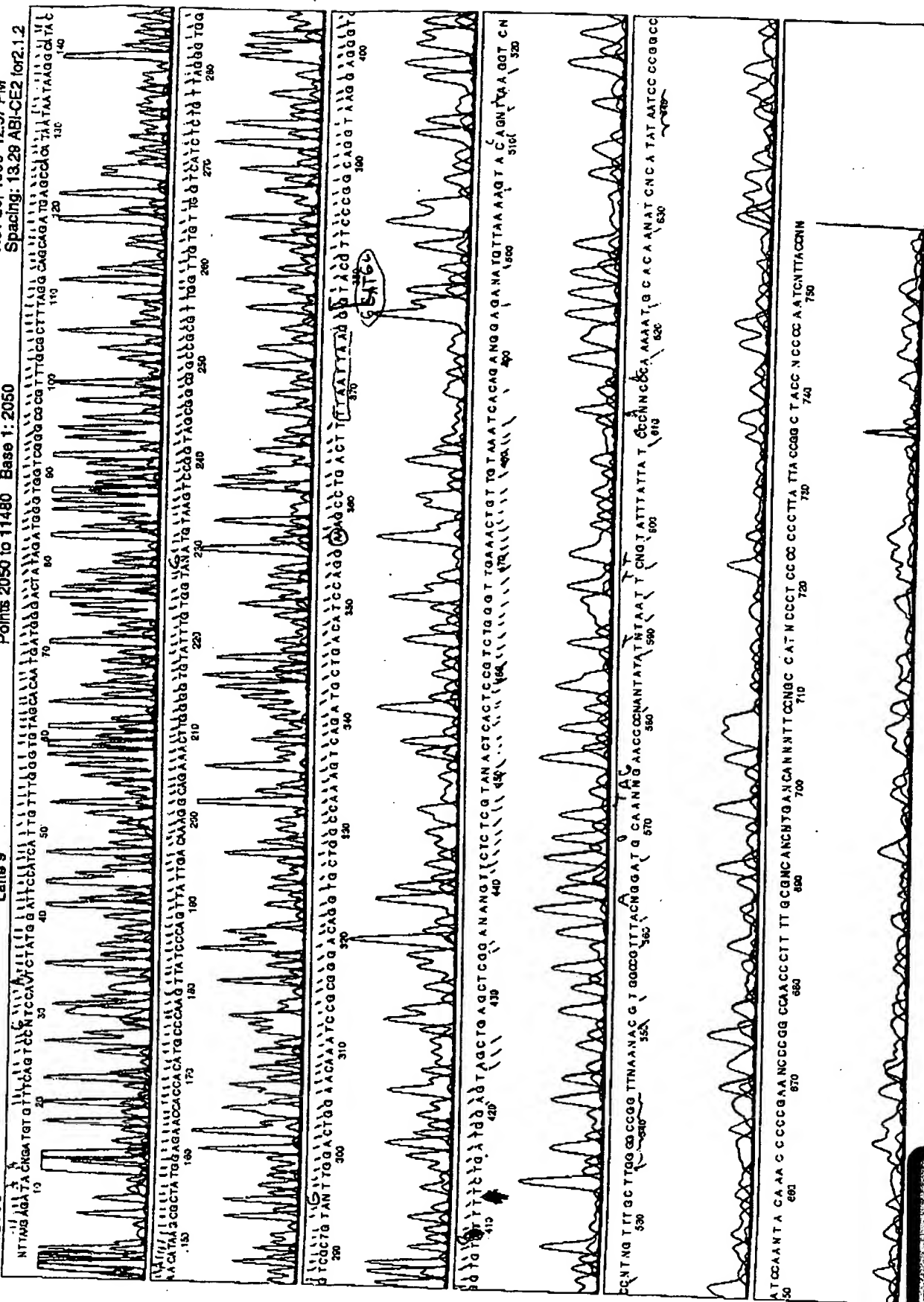
Nov 26, 1996 9:54 AM
Nov 26, 1996 6:57 AM
Spading: 12.96 ABI-CE2



Spacing: 14.02 ABI-CE2 for 2.1.2



Nov 26, 1996 3:28 PM
Nov 26, 1996 12:37 PM
Spacing: 13.28 ABL-CE2 for 2.1.2



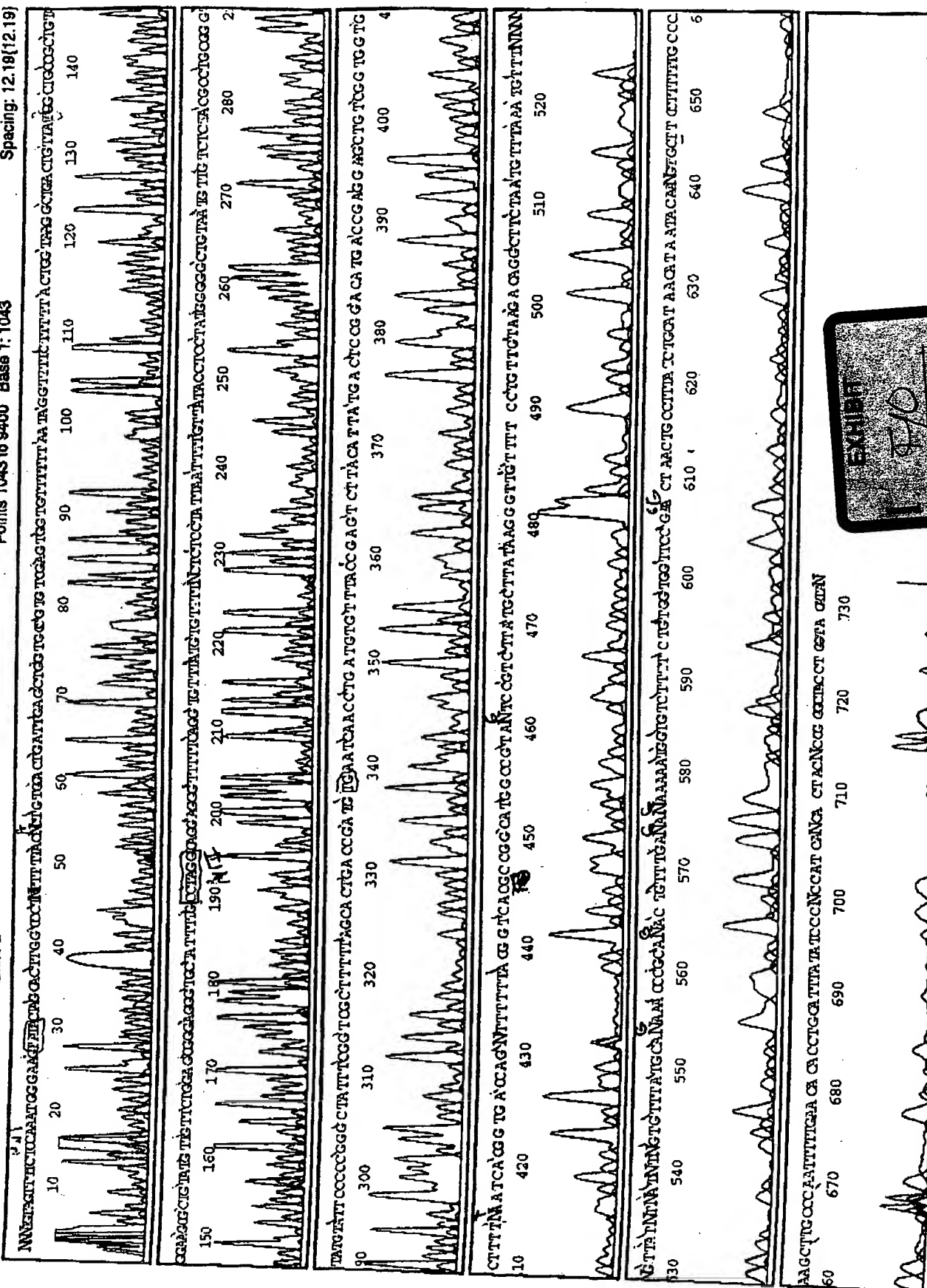
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Spacing: 11.90/11.90/R



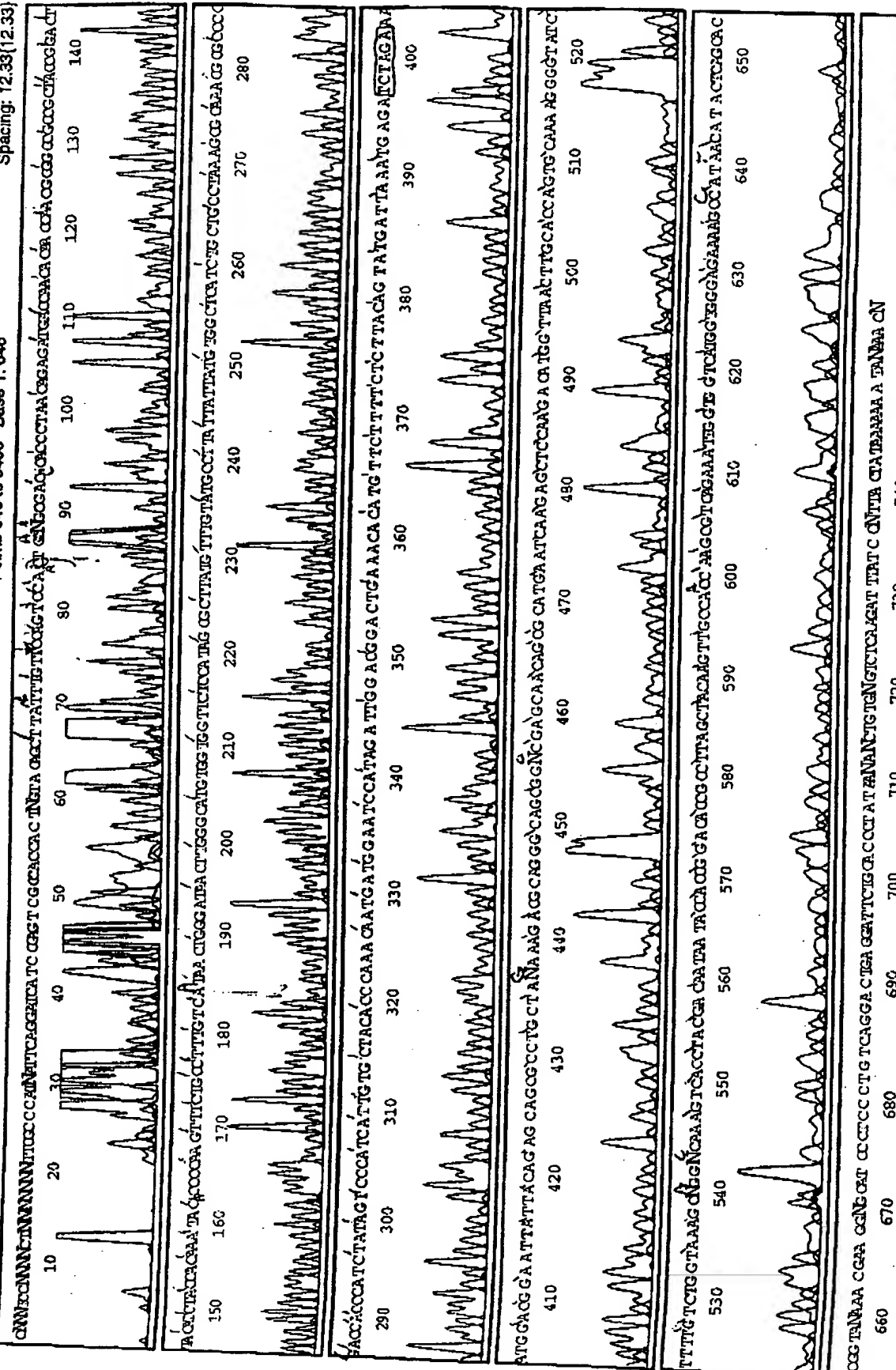
Signal G:639 A:858 T:543 C:294
DT POP6
pop6 dt-septre-stds.mtx
Points 1043 to 9400 Base 1:104

Page 1 of 1
Thu, Mar 20, 1997 10:22 PM
Thu, Mar 20, 1997 7:47 PM
Spacing: 12.18[12.19]



915

9



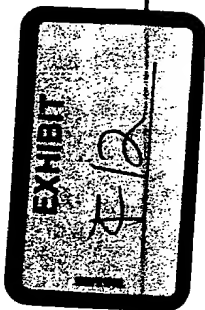
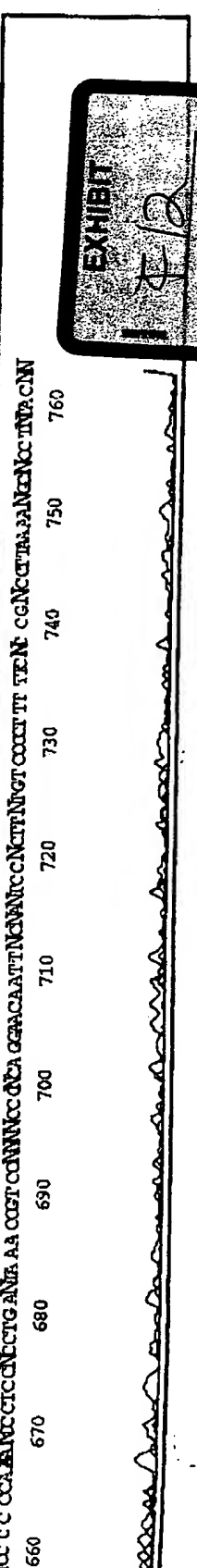
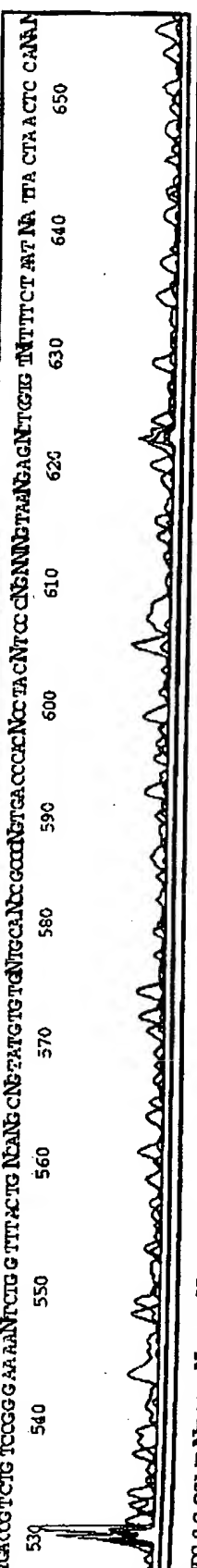
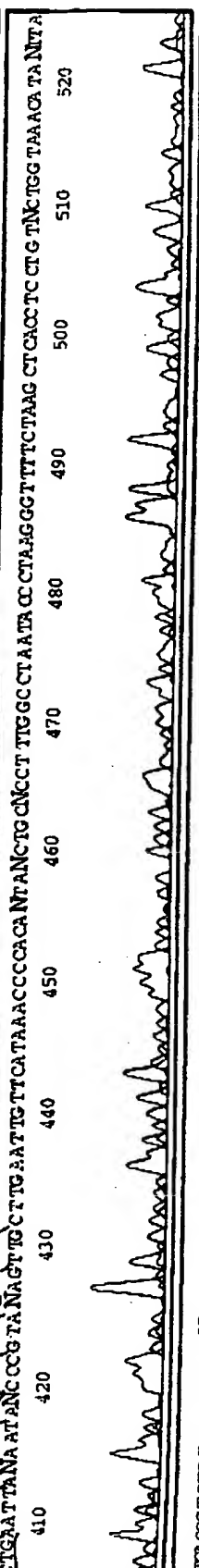
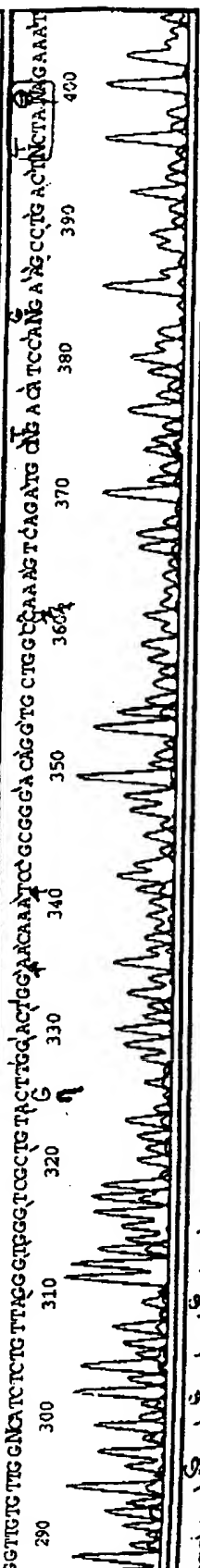
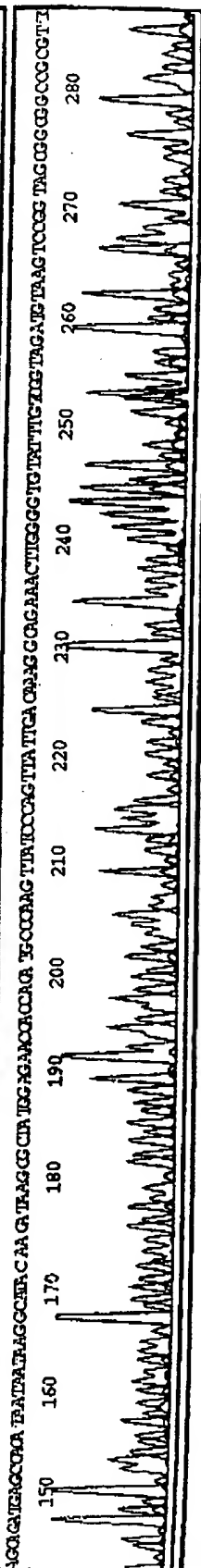
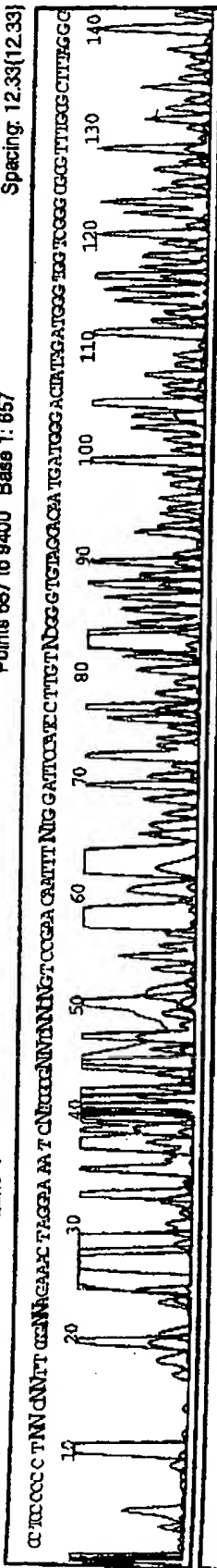
Model 310
Version 3.0
ABI-CE2 3.0
Version 3.0b1

A7-Wold-12
Wold-12
Lane 4

Signal G:251 A:255 T:160 C:128
DT POP6
pop6 dt-seprie-stds.mtx
Points 657 to 9400 Base 1: 657

Page 1 of 1
Fri, Mar 21, 1997 3:32 AM
Fri, Mar 21, 1997 12:57 AM
Spacing: 12.33(12.33)

67D 12
(p III, primer 435)



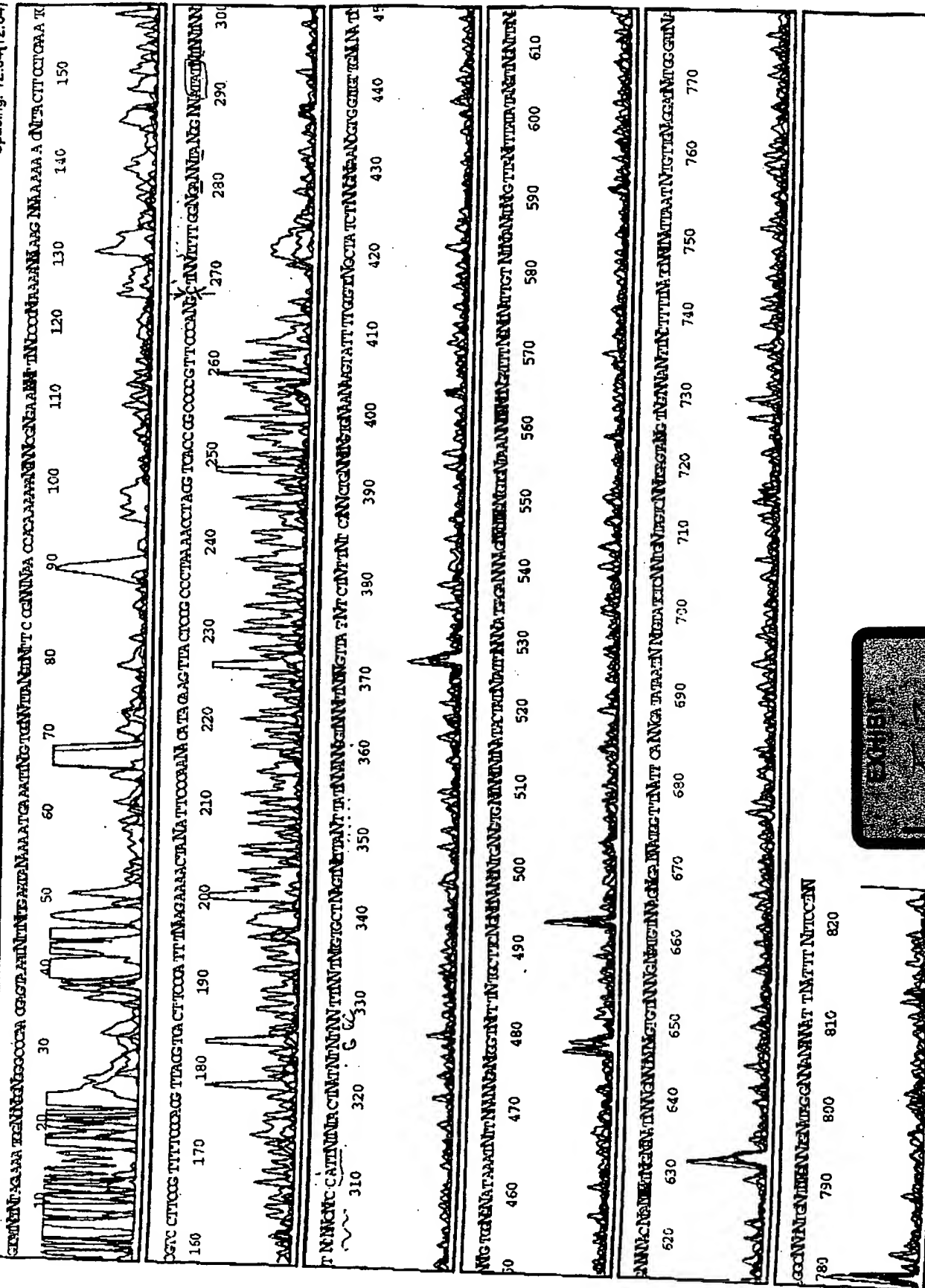
ABI
PRISM
Model 310
Version 3.0
ABI-CE2 3.0
Version 3.0b1

A1-Kostya/Wold-14
Kostya/Wold-14
Lane 1

0646(1,
primers KD10.

Signal G:71 A:84 T:75 C:57
DT POP8
pop8 dt-septre-sids.mtx
Points 1108 to 9400 Base 1: 1108

Page 1 of 1
Mon, Apr 21, 1997 12:49 PM
Mon, Apr 21, 1997 9:22 AM
Spacing: 12.64(12.64)



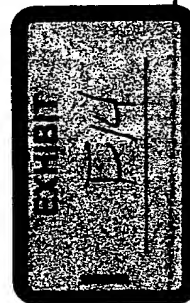
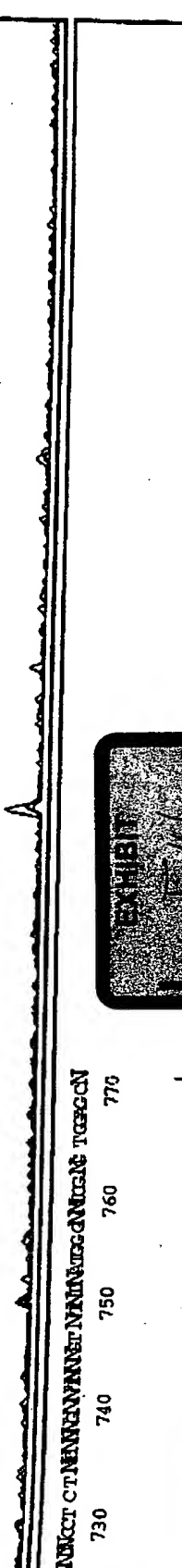
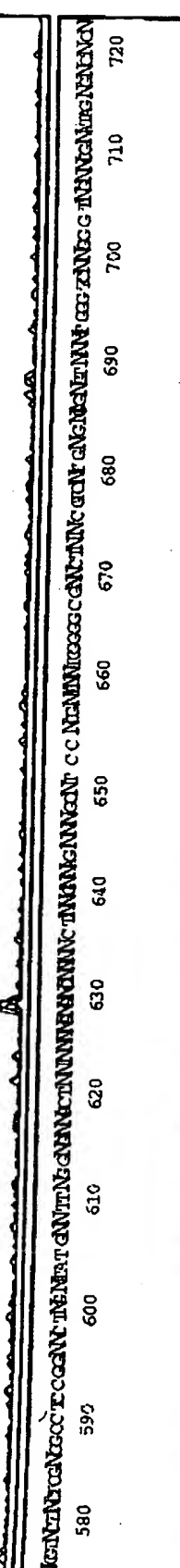
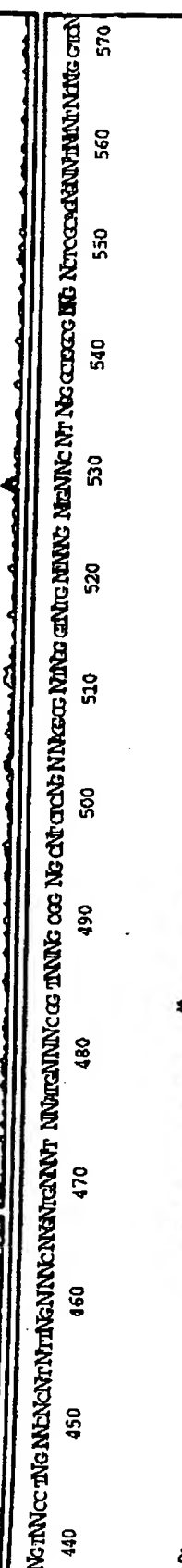
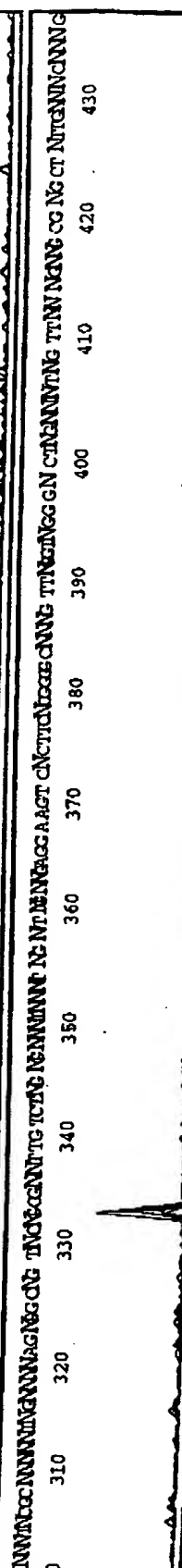
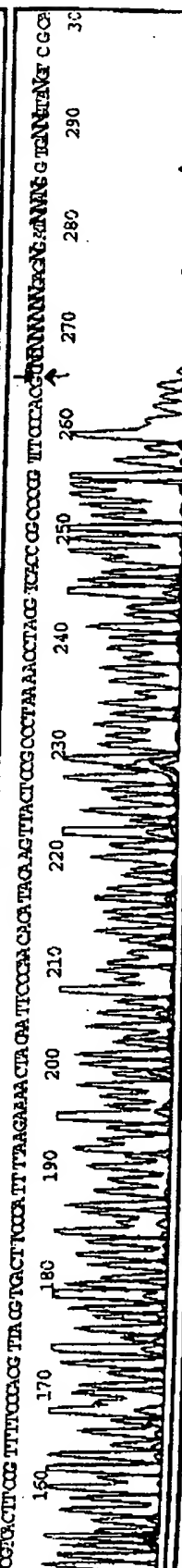
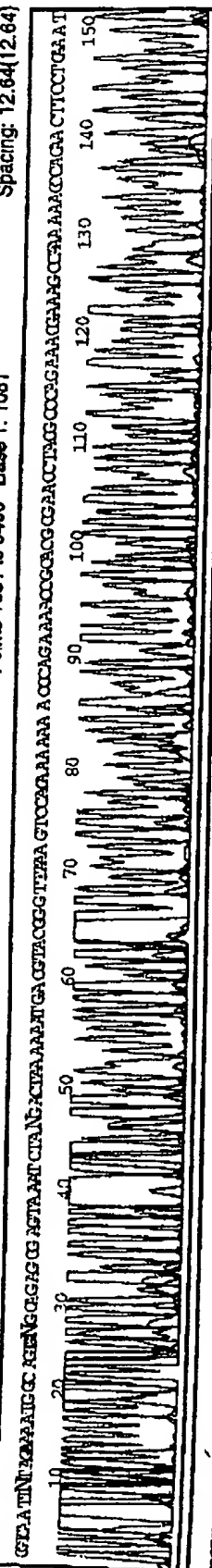
ABI
PRISM

Model 310
Version 3.0
ABI-CE2 3.0
Version 3.0b1

A3-Kostya/wold-15
Kostya/wold-15
Lane 2

Signal G:151 A:330 T:175 C:161
DT POP8
pop6 di-seprie-stds.mlx
Points 1081 to 9400 Base 1: 1081

Page 1 of 1
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Mon, Apr 21, 1997 12:07 PM
Spacing: 12.64(12.64)

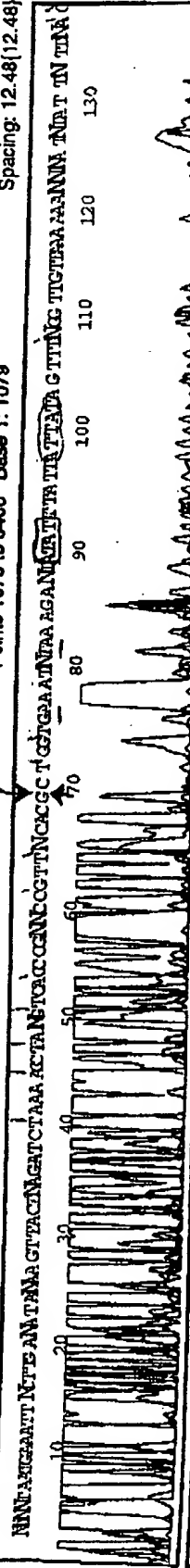


Model 310
Version 3.0
ABI-CE2 3.0
Version 3.0b1

A5-Kostya/wold-16
Kostya/wold-16
Lane 3

Signal G:99 A:145 T:99 C:92
DT POP8
pop8 di-septe-stds.mtx
Points 1079 to 9400 Base 1: 1079

Page 1 of 1
Mon. Apr 21, 1997 5:18 PM
Mon. Apr 21, 1997 2:42 PM
Spacing: 12.48(12.48)



140 150 160 170 180 190 200 210 220 230 240 250 260 270

280 290 300 310 320 330 340 350 360 370 380 390 400 410 420

430 440 450 460 470 480 490 500 510 520 530 540 550 560

570 580 590 600 610 620 630 640 650 660 670 680 690 700 710

720 730 740 750 760 770 780

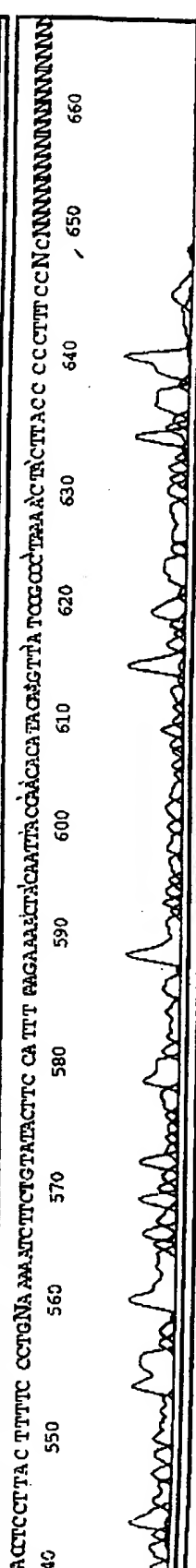
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1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000



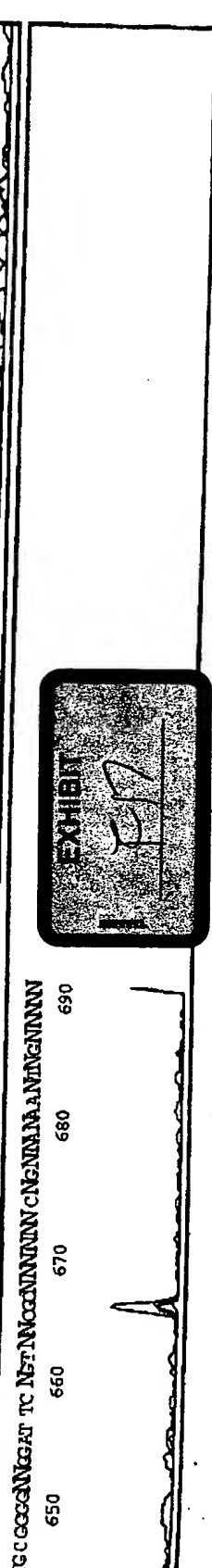
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Mon, Apr 21, 1997 5:17 PM
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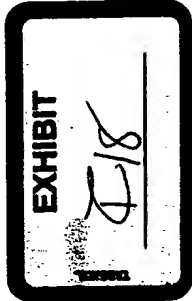
DATE	DESCRIPTION	AMOUNT	BALANCE
670	680	690	700



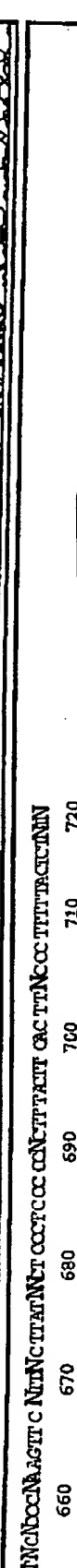
Page 1 of 1
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Page 1 of 1
Mon, May 12, 1997 10:24 AM
Mon, May 12, 1997 7:49 AM
Spacing: 12.64(12.64)



Page 1 of 1
Mon, May 12, 1997 1:00 PM
Mon, May 12, 1997 10:24 AM
Spacing: 12.19{12.19}



5/9

Page 1 of 2
Wed, Mar 24, 1999 1:30 AM
Tue, Mar 23, 1999 10:45 PM
Spacing: 12.04(12.04)

[illegible]

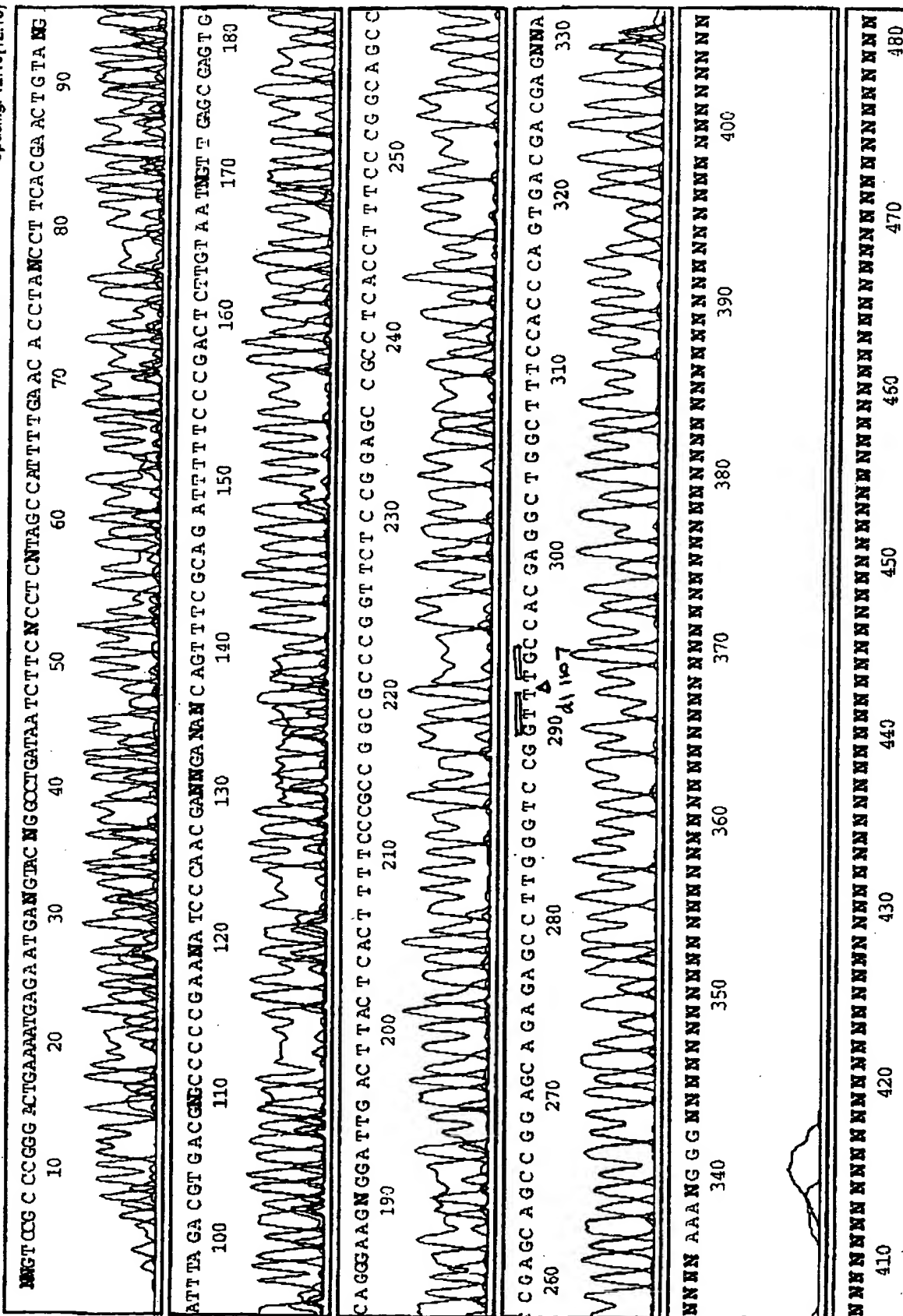
22

ABI
PRISM™

Doronin #5
Doronin #5
Lane 8

PCR product - 403, 4016-19
 Sequence = primer 4018 (dir) dRhod2
 Signal G:2100 A:1616 T:1484 C:2125
 DT POP6(BD Sat-Any Primer)
 Points 1114 to 10200 Base 1: 1114

Page 1 of 2
Wed, Mar 24, 1999 9:45 AM
Wed, Mar 24, 1999 7:00 AM
Spacing: 12.19{12.19}



EXHIBIT

222

Page 1 of 2
Wed, Mar 24, 1999 12:09 PM
Wed, Mar 24, 1999 9:45 AM
Spacing: 12.04{12.04}



13

ABI
PRISM
Model 310
Version 3.0
ABI-CE1
Version 3.0

Doronin #7
Doronin #7
Lane 2

pl2, primer 20 (dir)

Signal G:98 A:89 T:77 C:107
DT POPE(BD Set-Any Primer)
dRhod2
Points 970 to 10200 Base 1: 970

Page 1 of 2
Wed, Mar 24, 1999 5:15 PM
Wed, Mar 24, 1999 2:30 PM
Spacing: 12.04(12.04)

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10 20 30 40 50 60 70 80 90 100 110 120

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
130 140 150 160 170 180 190 200 210 220

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
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430 440 450 460 470 480 490 500 510 520

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
530 540 550 560 570 580 590 600 610 620

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
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730 740 750 760 770 780 790 800 810 820

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
830 840 850 860 870 880 890 900 910 920

TTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT TTTTCTTTT
930 940 950 960 970 980 990 1000 1010 1020

Page 1 of 2
24, 1999 8:01 PM
Wed, Mar 24, 1999 5:15 PM
Spacing: 12.04(12.04)

970619 Infection of A549 (Kostya's Virus)A549 (6/18) "1-40" - ~80% confl. (estimate 10^6 cells/TD)

Added SF-DME (2ml), removed & added 1ml SF-DME (~11Am);

Infection at 2:30 pm

<u>Virus</u>	<u># prep</u>	<u>Titer</u>	<u>Inf. Volume</u> (1:20 dilution)	<u># TD</u>
① mock	—	—	—	1
② dl 309 (VS 119) (970308)	—	1.2×10^{11}	10 μ l/TD	4
③ KD-1 (^{1101/1107} ADP) (970508)	—	9.64×10^{10}	15 μ l/TD	4
④ KD-2 (970611)	—	estim 4.5×10^{10}	20 μ l/TD	4
⑤ KD-3 970617 ^{~15me} 32g sup	—	estimated $2-3 \times 10^{10}$	{ 25 μ l/TD 40 μ l/TD	3 1 (Ara-C TD)
		150 cm ² flask		

Added 1 1/2 ml DME (10% FCS) at 3:30 pm.

Added 4X Ara-C (^{10 μ l of stock}) at ~6 pm & again at 9 AM on (6/20), fixed Ara-C & one set of coverslips at 27h post-infr. (other ss's fixed at 49 hours post-infection → all fixed in Paraformaldehyde followed by MeOH/DAPI, then a 2 min MeOH rinse & rehydrated in PBS; stained on (6/23) [after checked out Baoling's antibodies]



970623

Immunofluorescence Staining

all fixed in PF/meth w DAPI

Set #1

(M73(1:2)
121531 (1:100 find))(600 μ l)

- 1 mock (Ara-C) slight backgrd (all α Ab)
 2 dl 309 (Ara-C) 400% inf'd; some Golgi
 3 dl 309 (27h) Golgi + speckled around nuclei
 4 KD-1 (Ara-C) 80-90% inf'd; some Golgi
 5 KD-1 (27h) much more than Ad5; very vesicular
 6 \downarrow (49h) all cells bright (all vesicular)
 7 KD-2 (Ara-C) 70-80% inf'd; some Golgi
 8 \downarrow (27h) more like Ad5, but some vesicles (intense stain)
 9 \downarrow (49h) more diffuse, some cells quite bright; + Golgi
 10 KD-3 (Ara-C) 50-60% inf'd; pretty similar to Ad5 (AC)
 11 \downarrow (27h) not too much staining
 12 \downarrow (49h) some cells brighter (again rather "diffuse")

Set #2 (α DBP / α Fib each 1:400)(250 μ l)

- 13 mock (49h) slight backgrd (esp. FITC)
 14 309 (27h) all nuclei stain for both
 15 KD-1 (49h) strong staining for both
 16 KD-2 \downarrow more stained for DBP
 17 KD-3 \downarrow fewer cells stained for Fib

A-549 (6/18) 1:40 (p100) - Inf'd (6/19)

volume of 1: dil: 309 (10 μ l), KD-1 (15 μ l), KD-2 (20 μ l), KD-3 (40 μ l (Ara-C), or 25 μ l)1st Ab(s): 50 μ l for 60 minutes;

PBS rinses: 70 min, 12 min;

2nd Ab(s): Goat α Rabbit FITC \rightarrow Goat α Mouse FITC (not preadsorbed)
 1:50 dilution of each
 50 μ l for 34 minutes;

PBS rinses: 6 1/2 min, 5 min;
 dd H₂O dip
 mounted in Elvanol w p-phenylenediamine



970(5/20) Plaque Assays (New Counts)

Virus	Dilution	Dish	5/26	5/28	5/30	6/2	6/4	6/6	6/8
① dl751	$.5 \times 10^{-8}$	A	76	74	Tmrc	→			
		B	65	66	Tmrc	→			
	$.5 \times 10^{-9}$	A	10	12	10	9	0	0	0
		B	5	6	bact.	5	0	0	Tmrc
		C	4	6	10	10	2	0	2
	$.5 \times 10^{-10}$	A	2	0	2	3	0	0	0
		B	0	0	0	0	0	0	0
		C	1	0	1	0	0	0	0

② dl707 (4/23/97)	$.5 \times 10^{-8}$	A	10	37	13	30	31	10	Tmrc
		B	6	37	15	17	26	11	Tmrc
	$.5 \times 10^{-9}$	A	3	3	2	2	2	5	0
		B	0	6	0	2	5	3 ^(bact)	bact
		C	0	2	0	0	12	9	2
	$.5 \times 10^{-10}$	A	0	0	0	0	1	0	0
		B	0	0	0	0	0	0	0
		C	0	0	3	0	1	0	0

③ dl707 (3/15/97)	$.5 \times 10^{-8}$	A	16	41	14	68	Tmrc	19	→
		B	44	51	15	47	Tmrc	28	→
	$.5 \times 10^{-9}$	A	2	2	2	8	13	3	0
		B	1	8	5	2	8	5	2
		C	0	2	2	9	14	6	2
	$.5 \times 10^{-10}$	A	0	0	0	0	1	0	0
		B	0	0	0	0	0	1	0
		C	0	0	0	0	0	3	0

EXHIBIT

44

970520 Plaque Assays

Virus	Dilution	Dish	5/26	5/28	5/30	6/2	6/4	6/6	6/8
④ PHE	$.5 \times 10^{-8}$	A	42	80					
		B	27	102	74	Tmtc			
	$.5 \times 10^{-9}$	B	37	102	78	Tmtc			
		A	1	8	16	12	4	0	Tmtc
		B	7	17	11	14	1	0	Tmtc
	$.5 \times 10^{-10}$	C	7	15	20	7	11	0	Tmtc
		A	0	0	4	1	2	1	2
		B	0	0	3	0	1	0	0
		C	0	2	2	2	0	2	0
	$.5 \times 10^{-8}$	A	Tmtc						
		B	Tmtc						
⑤ KD	$.5 \times 10^{-9}$	A	20	8	8	3	5	0	0
		B	37	7	2	1	2	0	0
		C	24	11	11	1	0	0	0
	$.5 \times 10^{-10}$	A	2	0	1	1	1	2	0
		B	0	1	0	0	0	1	0
		C	5	0	0	2	1	2	0

EXHIBIT

#5

Cumulative Counts

970(5/20) Plaque Assays

Virus	Dilution	Dish	5/26	5/28	5/30	6/2	6/4	6/6	6/8
① dl751	$.5 \times 10^{-8}$	A	76	150	TMTc	→			
		B	65	131	TMTc	→			
	$.5 \times 10^{-9}$	A	10	22	32	41	41	41	41
		B	5	11	11	16	16	16	16
		C	4	10	20	30	32	32	34
	$.5 \times 10^{-10}$	A	2	2	4	7	7	7	7
		B	0	0	0	0	0	0	0
		C	1	1	2	2	2	2	2
			22	46	69	96	98	98	100
② dl707 (4/23/97)	$.5 \times 10^{-8}$	A	10	47	60	90	121	131	TMTc
		B	6	43	58	75	101	112	TMTc
	$.5 \times 10^{-9}$	A	3	6	9	11	13	18	18
		B	0	6	6	9	14	17	17
		C	0	2	2	2	14	23	25
	$.5 \times 10^{-10}$	A	0	0	0	0	1	1	1
		B	0	0	0	0	0	0	0
		C	0	0	3	3	4	4	4
			3	14	20	25	46	63	65
③ dl707 (3/15/97)	$.5 \times 10^{-8}$	A	16	57	71	139	TMTc	→	
		B	44	95	110	157	TMTc	→	
	$.5 \times 10^{-9}$	A	2	4	6	14	27	30	30
		B	1	9	14	16	24	29	31
		C	0	2	4	13	27	33	35
	$.5 \times 10^{-10}$	A	0	0	0	0	1	1	1
		B	0	0	0	0	0	1	1
		C	0	0	0	0	0	3	3
			3	15	24	43	79	97	101

EXHIBIT

H6

970520 Plaque Assays

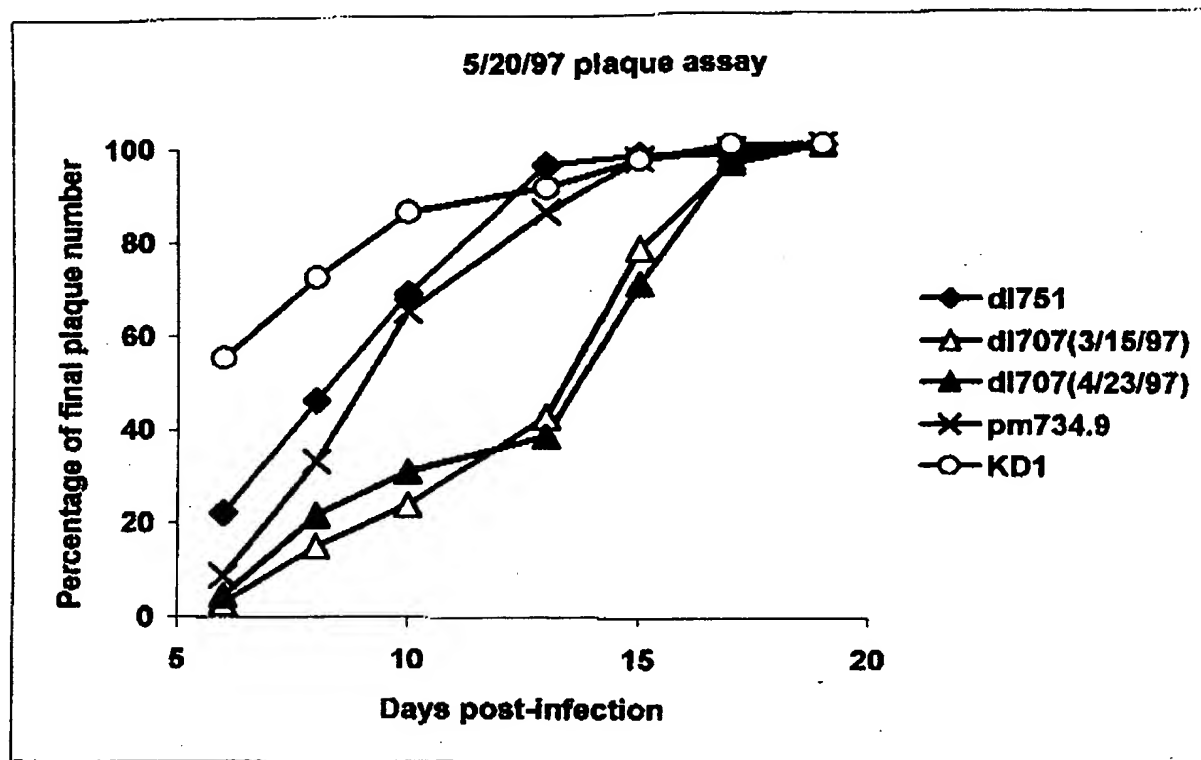
Virus Dilution	Dish	5/26	5/28	5/30	6/2	6/4	6/6	6/8
④ PmE $.5 \times 10^{-8}$	A							
	A	42	122	196	TmTC			→
	B	37	139	217	TmTC			→
	A	1	9	25	37	41	41	TmTC
		7	24	35	49	50	50	TmTC
		7	22	42	49	60	60	TmTC
	B	0	0	4	5	7	8	10
		0	0	3	3	4	4	4
		0	2	4	6	6	8	8
	C	15	57	113	149	168	171	173
	A	TmTC						→
		TmTC						→
⑤ KD $.5 \times 10^{-8}$	B							
	A	20	28	36	39	44	44	44
		37	44	46	47	49	49	49
		24	35	46	47	47	47	47
	B	2	2	3	4	5	7	7
		0	1	1	1	1	2	2
		5	5	5	7	8	10	10
	C	88	115	137	145	154	159	159

EXHIBIT

#7

970520 plaque assay*

	6	8	10	13	15	17	19
dl751	22	46	69	96	98	98	100
dl707(3/15/97)	3	14.9	23.8	42.6	78.2	98	100
dl707(4/23/97)	4.6	21.5	30.8	38.5	70.8	98.9	100
pm734.9	8.7	32.9	65.3	88.1	97.1	98.8	100
KD1	55.3	72.3	88.2	91.2	98.9	100	100

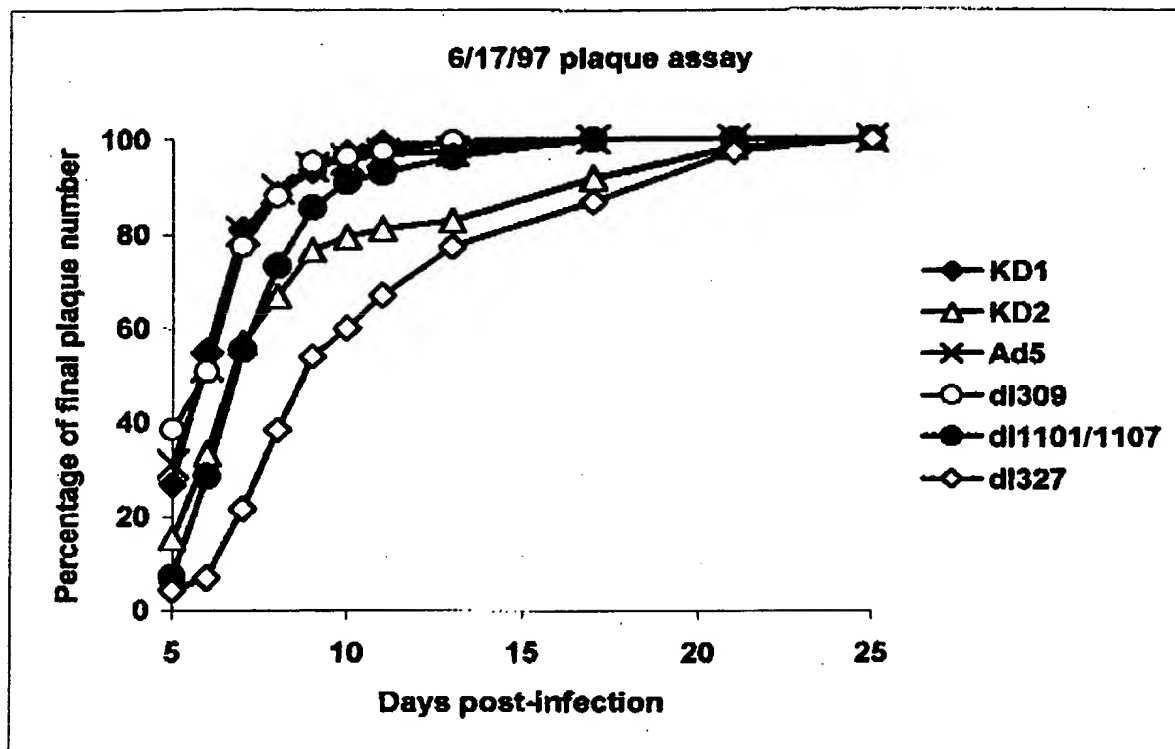


*numbers at the top of the page are the data points represented in the graph

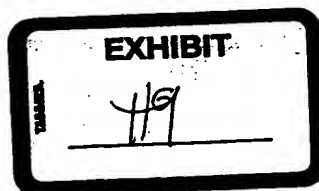


970520 plaque assay*

	5	6	7	8	9	10	11	13	17	21	25
KD1	27	55.2	80.9	88.4	93.4	97.1	99.2	99.2	100	100	100
KD2	15.3	33.3	56.8	66.7	76.6	79.3	81.1	82.9	91.9	98.2	100
Ad5	31.2	51.9	80.6	89.5	94.1	95.8	97	97.5	100	100	100
dl309	38.5	50.8	77.5	88.1	95.1	96.3	97.5	99.6	100	100	100
dl1101/1107	7.1	28.6	55.4	73.2	85.7	91.1	92.9	96.4	100	100	100
dl327	4.3	7	21.7	38.3	53.9	60	67	77.4	87	97.4	100



*numbers at the top of the page are the data points represented in the graph



(7/26) Blue

(5/28) Green

H6

970526

(5/20) Plaque Assays

<u>Virus</u>	<u>Dilution</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>Comments</u>
① dl751	0.5×10^{-8} $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	76+74 10+12 2+0	65+66 5+6 (bact.) 0°	4+6 1+0	quite large + very distinct
② dl 707 (4/23)	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	10+37 3+3 0°	6+37 0+6 0°	0+2 0°	small, flat + very indistinct
③ dl 707 (3/15)	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	16+41 2+2 0°	44+51 1+8 0°	0+2 0°	flat + <u>indistinct</u>
④ PME	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	46+80 1+8 0°	37+102 7+17 0°	7+15 0+2	fairly large + quite distinct
⑤ KP	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TNTC 20+8 2+0	TNTC 37+7 0+1	24+11 5+0	small to large all distinct; "cleared" center in many plaques (all cells lysed?)
⑥ mock	—	0	0	—	

AT Counts + descriptions
of Shari O'Briens
(5/20) Plaque Assay

Comments most likely done on
15/1/1

EXHIBIT

H10

Analysing the infectivity of the viruses 1101/1107 and d1309
on Growth arrested and growing cells.

cell line = HEL 299 human Lung embryonic.

Grown as in ATCC literature

T. 75 flask 1 from Karl,

split to 1:30 = 35 mm dish.
1:60 = 35 mm dish. (how many)
(for growing condition)

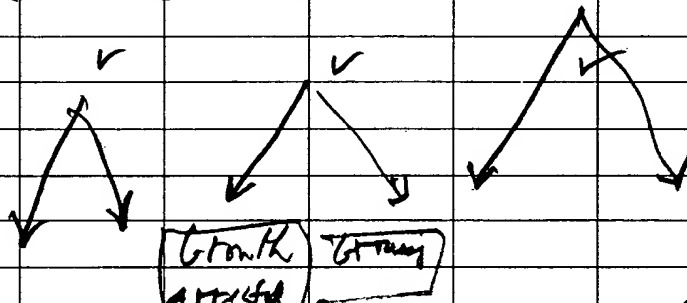
35 mm dish.

uninfected

1101/1107

d1309

1) 35mm + cover glass



how many days? 2 2
6 days

Growth
arrested

Growth

6

6

6

6

28

2) 35mm + coverslip =

how many days? 6 days

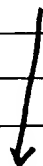
titer each point 1-6 days or

EXHIBIT

II

Analysis of the dl 1101/1107, dl309 viruses infectivity on Growth arrested and growing HEI 293 cells:

HEI 293 on T-75



35 mm dish

1:30 split for growth arrested

1:60 for growing cells

Growing growth arrested

1+2

1. Uninfected - mock

2. 1101/1107 infected

3. dl 309 infected

2

2

(12)

2

2



look for CPE - days?

4. On cover slip 1, 2, 3
(1+2)

days for Ad fiber IF.

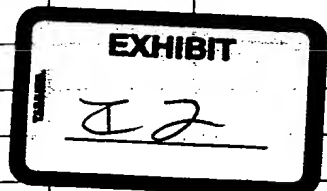
(10)

(22)

virus location

dl 309 = pfu ✓

dl 1101/1107 = pfu ✓



HEL 299

↓ 7.75

35 mm dishes 1:30,
↓ 1:60

MEM; 0.1 mM Non essential a.a.s; 1 mM Sodium-
pyruvate + 0.1 % lactalbumin hydrolysate.
+ 10 % FBS

↓
1:60 Split, count the cells + infect E
dl 110/11071, dl 309, 100 moi

↓
1:30 Split, allow to become confluent, then growth
arrest by low serum, (3 days) then infect E dl 1101/dl
dl 309 0.2% 1107

↓

EXHIBIT

43

viral infection dl 1101/1107

- count one growing MEL 299 cells.
- 100 pfu -

- Make 200 ml EMEM + Na Pyruvate, NEAA + Lactalbumin hydrolysate
100x 100x 100x

$$\frac{116}{81} = 1.47 \times 2 = 2.94 \quad \boxed{294,000 / \text{ml}}$$

dl 309 - 950111 - pfu 2.15×10^{11} Location 5-7

dl 1101/1107 - from Karl - pfu 1.95×10^{11}

from 35 mm - MEL 299 growing cells - counted = 294,000 / ml

$$100 \text{ pfu dl 309} = \frac{100 \times 294,000}{2.15 \times 10^4} = 1367.44$$

$$= \frac{294}{2.15 \times 10^4} = 0.00001367$$

= virus is too concentrated.
dilute to 10^9

10 ml dilute to 1 ml in medium (no serum) gives
- 2.15×10^9

EXHIBIT

24

$$= \frac{100 \times 294,000}{2.15 \times 10^4} = 1367.44$$

d1101/d1107 100 pfa =

~~100~~ x 294,000

294

dilute the virus to 10^4
in 10 μ l to 1 ml

1.95×10^4

1.95×10^4

= 15 μ l

12/16/96

Growing cells

2 x 35 mm dish d1309, 100 pfa

2 x 35 mm dish d1101/1107, 100 pfa

6 x 35 mm on coverslip d1101/1107 100 pfa

EXHIBIT

75

Growth arrested HEL 293 = infectious dil³ 10⁹,
dilution 1/10⁷

35 mm dish Medium + 0.29 FCS - 3 days

cell counts = 341,000

$$\text{dil } 10^8 = 100 \text{ pfa} = \frac{341 \times 10^3 \times 10^8}{2.15 \times 10^9} = \frac{15.8}{\text{ml}}$$

$$\text{dil } 10^6 = 100 \text{ pfa} = \frac{341 \times 10^3 \times 10^6}{1.95 \times 10^9} = \frac{17.4}{\text{ml}}$$

Viral 10 ml to 1 ml $\rightarrow 10^9$

↓
then 37°C / 1 hr

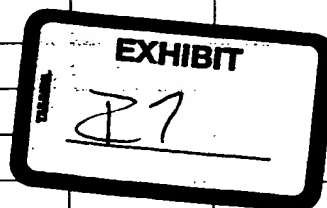
↓
Medium + 0.29 FCS

EXHIBIT

26

Fixing the HEL299 cells + Methanol + DAPI (1^{mg}/ml)
(1^{µl} to 1ml methanol)

1. Wash the cells 2x PBS w/o
 2. Fix + Methanol (-20°C) + DAPI ~ 8 min (-20°C)
 3. Wash in Methanol w/o DAPI
 4. Wash in 1x PBS, store at 4°C
-
- | | | | | |
|-----|------------------|----------|--------|---|
| ✓ | 1 day | 12/11 | | |
| ✓ | 2 day | 12/18 | | |
| ✓ | 3 day | 12/19/96 | → | 2 d1309 started showing CPE |
| ✓ | 4 day | 12/20 | NO CPE | |
| | 5 " | 12/21 | NO CPE | - d1309 complete CPE |
| | 6 " | | | |
| | 7 day | 12/23 | NO CPE |) all d1309 cells infect rounded & lame |
| | 8 day | 12/24 | NO CPE | |
| | 9 " | 12/25 | | |
| → | 10 day | 12/26 | CPE?! | cells looks different vs d1101/1107 |
| F | 11 | 12/27 | | |
| S | 12 | 12/28 | | |
| Sm | 13 | 12/29 | → | CPE? starts on 12 th day d1101/1107 |
| ✓ M | 14 | 12/30 | → | CPE? spreads - d1101/1107 |
| | 15 | 12/31 | | " " |
| | 16 | 1/1/97 | | |
| ✓ | 17 | 2/1/97 | → | Take photographs |
| | 18 | 3/1 | → | |
| | 19 | 4/1 | → | |
| | 20 | 5/1 | → | almost all the cells died - d1101/ |
| | | | | |
| | 25 th | 12/1 | → | Stain - dish, 2 crystal violet
2 d1101/1107
2 - d1309 |



Growth arrested HEL 299 cells:

Date	Days	
8	15	No visible CPE in all 1101 (1107) : Some cells are floating. In normal HEL 299 cells some cells are floating but less.
9	16	Some as above.
10	17	"
11	18	same
12	19	cells looking different than norm
13	20	HEL 299 But "d1809 CPE looks different
14	21	"
15	22	" CPE?!
16	23	" CPE?!
17	24	
18		

EXHIBIT

I 8

HEL299 cells

Kodak

17 days

7

Tmax 100
~~black & white print~~Growing HEL 299:

1.	mock	N
2	"	+1
3	"	-1
4	"	-1
5	"	N
6	"	+1
7	dl 1101/1107	N
8	"	+1
9	"	-1
10	"	N
11	"	+1
12	"	-1
13	"	N
14	"	+1
15	"	-1
16	"	N
17	"	+1
18	"	-1
19	"	N
20	"	+1
21	"	-1
22	"	N
23	"	+1
24	"	-1
25	"	N
26	"	+1
27	"	-1
28	"	N
29	"	+1
30	"	-1
31	"	N
32	"	N
33	"	+1
34	"	-1
35	mock	N
36	mock	+1



EXHIBIT

29

IF: HEL 299: Growing:

1. ab - Filter, → 1:400 } 30'
- DBP → 1:400
2. Goat anti mouse Rhodamine 1:50 (not preabsorbed)
- Goat anti Rabbit FITC 1:25

- 1 = 1st layer
- 2 = 2nd
- 3 = 3rd
- 4 = 4th
- 5 = 14th
- 6 = 17th
- 7 = CTRL

811101/1107

2 DBP

p 67

66420

850625

2 Ad2 Fiber

4 D2-5

ascites fluid

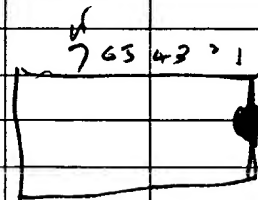
1. ab = Ad Fiber
- = DBP

dil 1:400
dil 1:400

in 1 tube

35 μ l / disk → 37°C / 30 min

↓ wash: 0 1x PBS w/o, 10 min x 3 times



123

2. Goat α mouse Rhodamine 1:50
- Goat α Rabbit FITC = 1:25

37°C / 15 min

960125

8 → 400
16 → 400

3764
54
16

12,

400

EXHIBIT

10

Growth Assay

Growth arrested cells

HEL 299

T-75 → split 15 x 35 mm dish.

dishes same like growing

↓
add EMEM + 0.2% FCS

↓
3 days

↓
infect \bar{e} [dl 1101/1107]
pm 975

the total dl 309

total dish # 27

EXHIBIT

211

HEL 299 T-25

Growth Assay

Growing:

↓ split to 35 x 35 mm dish

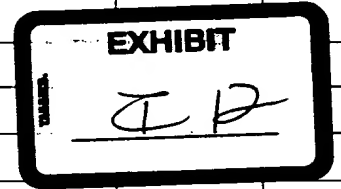
① 1 + 10 dish days (1, 4, 6, 8, 10, 12, 14, 16, 18, 20)
dl 1101/1107

② 1 + 10 dish Same days - pm 975

↓ infect 100 pfu, freeze the dishes as days shown.

③ 4 dishes infect e dl 309 for tuc infection
Freeze 1, 4, 6 days.

the dishes 27



1/14/98

Infection	dl 1101/1107	pfu 1.95×10^{11}
	dl 309	2.15×10^{11}
	pm 975	4.06×10^{10}

Growing HEL 299 cells counted: 212,000/ml

①

100 pfu

For dl 1101/1107 = $\frac{100 \times 2.12 \times 10^5}{1.95 \times 10^9} = \frac{2.12}{1.95 \times 10^2} = 10.8$
 Dilute the virus to 10^9
 10 ml to 1 ml medium No serum

②

For pm 975

= $\frac{100 \times 2.12 \times 10^5}{4.06 \times 10^9} = \frac{2.12}{4.06 \times 10^2} = 5.2$
 Dilute the virus to 10^9
 50 ml to 500 ml serum free media

Growth Curve

Growing cells (Summary)

(3) true control

virus dil 309.
 dilute the virus to 10^9
 10 μ l to 1ml serum free
 medium

$$= 10^6 \times 2.12 \times 10^6$$

$$2.15 \times 10^7 \times 2$$

$$= \frac{2.12}{2.5 \times 10^2} = 9.8 \mu$$

1. Wash the cells in PBS w/o.
2. infect in serum free medium 37C / 1 hr
3. After 1 hr, remove the medium, wash in lx medium
4. Add MEM + 10% FCS.

Freeze the cells after

1-17-97	1 day	(G1)	1/15/97 ✓
	3 day	(G2)	dil 309, pm 975 shows CPE NO CPE in dil 1101/1007
1-19/97	5	(G3)	N 40% CPE in pm 975 NO CPE in dil 1101 -
	6	(G4)	pm 975 ✓ NO CPE in dil 1101
	7	(G5)	pm 975 ~ 100% ✓ (G3 dil 1101/1107 ~ CPE? - NO)
10	10		pm 975 dil 1101/1107 (NO CPE 40%) dil 309 (photos)
	15		dil 1101/1101 (morphology change CPE?)
	24		dil 1101/ G5

EXHIBIT

I B

Growing II

7

infected		1/31/97							
		100	500	100	500	1	100	500	
		d1309	SEP 16	PM 975		d11101	d107		
Day 2		NO CPE	"	NO CPE	"	NO CPE	"		
Day 2		Few cells	Few	Few	Few	NO CPE	"		
		rounds	rounds	rounds	rounds				
Day 3		10% CPE	-20% CPE	20%	50% CPE	NO CPE			
Day 6		100% CPE in		PM 975; d1309					
		NO CPE in		d11101/1107					
Day 14			—	—		500 pfu - CPE	starts.		
Day 17			—	—		100 pfu - CPE starts			
						500 pfu - CPE ++			

EXHIBIT

714

Growth Arrested

MEL 288

22/51

G1

Days

3

pm 975 - -70 C

5

pm 975, dl 1101/1107, dl 389 (photos)

7

pm 975 -70 C (photos)

10

pm 975; dl 1101/1107 (NO LPE)

(GAT)

(GAT)

14

pm 975

(GAT)

15

-pm 975 AND CME.

521 cells from control & pm 975. dl 1101/1101
are same off. NO contamination.
May be due to not changing medium?

19

pm 975 (GAT)

EXHIBIT

15

Growing cells
on cover slips
for IF & CPE

HEL 299 cells

counted 1 dish = 188,000 cells. (1:35 dil)

① virus pm 925 pfu 4.06×10^{10}

$$\text{for } 100 \text{ pfu} = \frac{100 \times 1.88 \times 10^4}{4.06 \times 10^2} = \frac{1.88}{4.06 \times 10^{-2}}$$

dilute the virus to 10^9 titer.

50 μ l to 500 μ l serum free media

$$= 4.6 \mu\text{l}$$

② virus dl 101/1107

$$= \frac{100 \times 1.88 \times 10^4}{1.95 \times 10^4} = \frac{1.88}{1.95 \times 10^{-2}}$$

dilute the virus to 10^9

10 μ l to 1ml medium.

$$= 9.6 \mu\text{l}$$

③ +ve control dl 309

$$= \frac{100 \times 1.88 \times 10^4}{2.15 \times 10^4} = \frac{1.88}{2.15 \times 10^{-2}}$$

dilute the virus to 10^9

10 μ l to 1ml medium

$$= 8.7 \mu\text{l}$$

40
10

EXHIBIT

2/6

Growth arrested HEL 299^{P12} cells P¹²

24 days

0	HEL 299 (mock)	= 0
1	"	+1
2	"	-1
3	"	0
4	"	+1
5	"	-1
6	HEL 299 + dl 1101/1107	= 0
7	"	+1
8	"	-1
9	↑	
10		
11		
12		
13		
14		
15		
16		
17		
18		
19		
20	↓	
	Growing cells	31 days
21	HEL 299 mock	= 0
22	"	+1
23	"	-1
24	+ PM 975	=
25	"	
26	"	
27	dl 1101/1107	
28	"	
29	"	
30	dl 309	
31	"	
32	"	
33	PM 975	
34	↓	
35		
36		
37	↓	

EXHIBIT

17

25/8/77
 GROWING EXPRESSION HEL-221
 infected E d1101/1107 24th day

	HEL 299 (mole)		TMV 400 B+W
1	HEL 299 (mole)	= 0	
2	"	+1	
3	"	-1	
4	"	0	
5	"	+1	
6	"	-1	
7	HEL 299 + d1104/1107	= 0	
8	"	+1	
9	"	-1	
10	"	0	
11	"	+1	
12	"	-1	
13	"	0	
14	"	+1	
15	"	-1	
16	"	0	
17	"	+1	
18	"	-1	
19	"	0	
20	"	+1	
21	"	-1	

print reads 0=1

Same

223

Growing 21, 22, 23 mole

	HEL 299 MOLE		
21	HEL 299 MOLE	= 0	
22	"	+1	
23	"	-1	
24	"	0	
25	+ PM 975	0	
26	"	+1	
27	"	-1	
28	d11101	0	
29	"	+1	
30	"	-1	
31	d1309	0	
32	"	+1	
33	"	-1	
34	PM 975	00	
35	"	+1	
36	"	-1	
37	"		

Growing cells 3rd day

Same

EXHIBIT

IB

Growth arrested HEL 299 cells

- Growth Curve: -

Count the cells: 347,000 cells

① 100 pfu = for dilution 10⁴

$$= \frac{100 \times 347,000}{1.95 \times 10^4} = \frac{347}{1.95 \times 10^4} = 17.2$$

dilute the virus to 10⁴
10 ml to 1 ml

② 100 pfu for pm 975

$$= \frac{100 \times 3.47 \times 10^4}{4.06 \times 10^4} = \frac{3.47}{4.06 \times 10^2} = 8.5$$

dilute the virus to 10⁴
50 ml to 500 ml

③ the count is 309

$$= \frac{100 \times 3.42 \times 10^4}{2.15 \times 10^4} = \frac{3.42}{2.15 \times 10^2} = 16$$

dil to 10⁴
10 ml to 1 ml

↓
work
infant
EMEM 0.29 FU

14

photographs:

Tmax 170 B/w

Growth arrested HEL299, 3 days

1	HEL299 - MOLA	= 0
2	"	+1
3	"	-1
4	"	0
5	"	+1
6	"	-1
7	+ pm 975	0
8	"	+1
9	"	-1
10	"	0
11	"	+1
12	"	-1
13	"	0
14	"	+1
15	"	-1
16	"	0
17	"	+1
18	"	-1

pm 975, 3rd day, 6A

nucleus appears darker than CNA

↓ KAT-

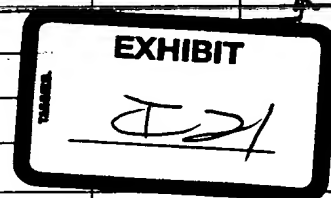
EXHIBIT
420

P IV
in photos

Growing 9th day

Tmax 100 B/w Prints

1	HEL 299 (Mock)	2 NCO	
2	"	+	
3	"	-1	
4	"	0	
5	"	+1	
6	"	-1	
7	dl 309	0	
8	"	+	
9	"	-1	CPE ✓
10	"	0	
11	"	+1	
12	"	-1	
13	pm 975	0	
14	"	+1	
15	"	-1	CPE ✓
16	"	0	
17	"	+	
18	"	-1	
19	dl 1101	0	
20	"	+1	0 ?
21	"	-1	0
22	"	0	
23	"	+1	
24	"	-1	
Growth arrested 5 th day			
25	HEL 299 Molk	0	
26	"	+1	
27	"	-1	
28	pm 975	0	
29	"	+1	
30	"	-1	CPE - Not yet
31	"	0	NO CPE sign
32	"	+	
33	"	-1	
34	dl 1309	0	
35	"	+	Shows - starting CPE
36	"	-1	
37	"	0 less CPE	



8/

Photographs

Carl took Growth Arrested HEL 255 9th day
1-18 photos

19	HEL - 6A -	0	}	NO CPE sign
20	"	+1		
21	"	-1		
22	PM 925	0		
23	"	+1		
24	"	-1		
25	"	0		
26	"	+	}	NO CPE sign
27	"	-1		
28	DI 1101	0		
29	"	+1		
30	"	-1		
31		0		
32		+		
33		-1	}	shows CPE.
34	DI 309	0		
35	"	+		
36	"	-1		
37	"	0		
38	"	+1?		

EXHIBIT
I 22

P6

photos:

Tmax 100 black & white

Growth arrested HEL 293 - 10th day.

1 HEL 299, GA, mock - 0

2 " " +1

3 " " -1

4 PM975 - 0

5 " " +1

6 " " -1

7 " " 0

8 " " +1

9 " " -1

10 dl 1101 / 1107 - 0

11 " " +1

12 " " -1

13 " " 0

14 " " +1

15 " " -1

16 dl 309 - 0

17 " " +1

18 " " -1

19 " " 0

20 " " +1

21 " " -1

ND CPE?

ND CPE.

shows CPE - growing

Growing cells → 15 days

22 HEL 293 mock - 0

23 " " +1

24 " " -1

25 PM975 - 0

26 " " +1

27 " " -1

28 dl 309 - 0

29 " " +1

30 " " -1

31 dl 1101 / 1107 - 0

32 " " +1

33 " " +1

34 dl 1101 / 1107 - 0

All the cells rounded & most of them floating (dead cells)

All the cells rounded & floating (dead)

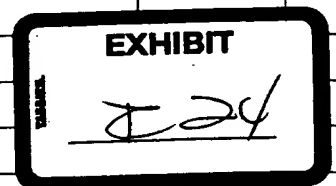
Cells are larger, fewer, some cells have larger nuclei - CPE?

EXHIBIT

223

photographs 3rd day
 Growing HEL 299 P¹⁷

1	HEL 299	0	0	
2	"	+1		
3	"	-1		
4	dl 309	100 pfn	0	
5	"	"	+1	100 pfn ~ 107 LPS
6	"	"	-1	
7	dl 309	500 pfn	0	
8	"	"	+1	500 pfn ~ 309
9	"	"	-1	
10	pm 975	100 pfn	0	
11	"	"	+1	
12	"	"	-1	100 pfn ~ 209
13	"	"	0	
14	"	"	+1	
15	"	"	-1	
16	pm 975	500 pfn	0	
17	"	"	+1	
18	"	"	-1	500 pfn ~ 919
19	"	"	0	
20	"	"	+1	
21	"	"	-1	
22	dl 1101	100 pfn	0	
23	"	"	+1	
24	"	"	-1	100 pfn NO LPS
25	"	"	0	
26	"	"	+1	
27	"	"	-1	
28	dl 1101	500 pfn	0	
29	"	"	+1	
30	"	"	-1	500 pfn NO LPS
31	"	"	0	
32	"	"	+1	
33	"	"	-1	
34	HEL 299	control	0	
35	"	"	+1	
36	"	"	-1	



P2

photographs

Growing 24th day:-

1	HEL 299, G	=	0
2	"		+1
3	"		-1
4	"		0
5	"		+1
6	"		-1
7	dl 1101 / 1107		0
8	"		+1
9	"		-1
10	"		0
11	"		+1
12	"		-1
13	"		0
14	"		+1
15	"		-1

skips (0)

[GA] HEL 299 19 days

16	HEL 299 GA	-	0
17	"		+1
18	"		-1
19	"		0
20	"		+1
21	"		-1

cells are skips

22	pm 925		0
23	"		+1
24	"		-1
25	"		0
26	"		+1
27	"		-1

28	dl 1101 /		0
29	"		+1
30	"		-1
31	"		0
32	"		+1
33	"		-1

34	HEL 299 C		0
35	"		+1
36	"		-1

EXHIBIT
225

Expt 3

Growth arrested 299 cells p¹⁷¹
- Growth curve:-

Count the cells: 347,000 cells

① 100 pfr =
for d1107/107 $= \frac{100 \times 347,000}{1.95 \times 10^4} = \frac{347}{1.95 \times 10^4} = 17.0$

dilute the virus to 10⁴
10 ml to 1 ml

500 pfr = 85.0

② 100 pfr
for pm 975 $= \frac{100 \times 3.47 \times 10^4}{4.06 \times 10^4} = \frac{3.47}{4.06 \times 10^2} = 8.5$

dilute the virus to 10⁴
50 ml to 500 ml

500 pfr = 42.5 ml

③ 400 CPE d1309 $= \frac{400 \times 3.47 \times 10^4}{2.15 \times 10^4} = \frac{3.47}{2.15 \times 10^2} = 16.0$

dil to 10⁴
10 ml to 1 ml

500 pfr = 80.0

EXHIBIT

226

↓

wash

infest

EMEM 0.29 FCS

Days 4 2 =

NO CPE

3/10/97
F

Days 3:

d1107, pm 975, d1309 NO CPE / 100 pfr
at 500 pfr, 2 pm 975 & d1309 shows
beginning of CPE

Day 4) = NO CPE 1107/1107 (100 & 500 pfr)

Day 5) = NO CPE PM 975 / 100 pfr

= CPE begins pm 975 500 pfr only

Day 6 = NO CPE PM 975 100 pfr

2/13/97

Day 7 = NO CPE d1107/100 & 500 pfr

NO CPE d1309 100 pfr. CPE in d1309 500 pfr

Growth Curve :- Frozen - days

KEI- 299

pm975,

dl 1101

Growing:

1, 3, 5, 6, 7,

1, 3, 5, 6, 7, 10, 15, 19

GA :

3, 5, 7, 10, 14

5, 7, 10

19

GA

pm975

GA:

✓ GA 3 = 14th day
✓ GA 4 = 10th day
~~GA 2 = 5th day~~
✓ GA 7 = 19th day
~~GA 1 = 3th day~~

Growing

✓ GA 3 = 3rd day 67
✓ GA 6 = 5th day
✓ GA 6 = 6th day 64
✓ GA 7 = 7th day

GA

dl 1101/1107

✓ GA 7 = 19th day
✓ GA 9 = 10th day
✓ GA 2 = 5th day
✓ GA 23 = 23rd day

Growing

GA 3 = 5th day
GA 4 = 15th day
GA 24 = 24th day

2/18/97

pm975:

GA = 10, 14, 19 day

Growing = 3, 5, 6, 17 day

307?

EXHIBIT

127

Growth Curve - Plaque assay:

293 cells:-

Growing = pm 975 : days 1, 3, 5, 6, 7

GA = pm 975 = 3, 5, 7, 10

#9

Growing = dl1101 = 1, 5, 7, 10, 15

GA = 7, 10

#7

dl309 =

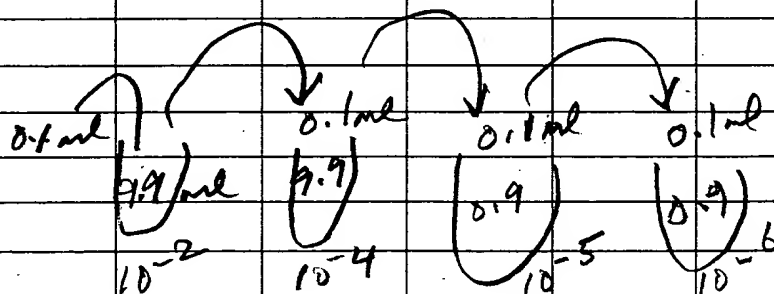
infections = 0.5 ml
0.1 ml

wt
10⁻²
10⁻⁴
10⁻⁵

DS pm 975 first
of points Growing =

5 = 5x = 25 dish
GA = 4 = 4x = 20 dish

35



0.5 ml adaptation:
1 ml 10⁻² to 10⁻⁶

0.1 ml wt

Strain on 2/24/97

EXHIBIT

228

dl 1101/1107 Growth Curve:
plaque assay

dl 1101/1107

GA:

Day

GA7 = 19

GA9 = 10

GA2 = 5

GA = 23

Growing

G3 = 5 hr

G4 = 15 hr

G24 = 24 hr

GA5 p0925

Dilutions

0.1 ml

9.9 ml

10^{-2}

0.1 ml

9.9 ml

10^{-4}

0.1

0.9

10^{-5}

0.1 ml

0.9

10^{-6}

↓

0.5 ml injection:

EXHIBIT

729

Growth Curve

3/4/97

21101/1207

100 pfu

Growing

Small plaques

went one more day:-

$$G3 = 5^{th} \text{ day} : 1.4 \times 10^4$$

$$15^{th} \text{ day} = 14^2 = 406 / 1 \text{ ml} \times 10^2$$

$$= 4 \times 10^4$$

$$24^{th} \text{ day} = 10^{-4} \quad 66 / 0.5 \text{ ml}$$

$$132 / 1 \text{ ml}$$

$$= 132 \times 10^4$$

$$= \boxed{1.3 \times 10^6} / \text{ml}$$

G4

$$5^{th} \text{ day} = 1.1 \times 10^3 \text{ pfu/ml (No plaques in ud.)}$$

$$10^{th} \text{ day} = 7 \times 10^2 / 0.5 \text{ ml} = 14 \times 10^2$$

$$= \boxed{1.4 \times 10^3}$$

$$19^{th} \text{ day} = 42 \text{ plaques} / 0.5 \text{ ml (Small)}$$

$$= 84 / 1 \text{ ml} \times 10^2$$

$$= \underline{8.4 \times 10^3} \text{ pfu/ml}$$

$$23^{th} \text{ day} = 28 \times 10^2 / 0.5 \text{ ml}$$

$$= 56 \times 10^2$$

$$= \underline{5.6 \times 10^3} \text{ pfu/ml}$$

EXHIBIT

130

Growth Curve:

2-25-97

<u>Growing</u>	<u>PM 975</u>	<u>180 pfu</u>	
<u>3rd day</u>	10^{-6}	<u>plaques</u> 71	<u>pfu/ml</u> 7.1×10^7
5 th day	10^{-6}	13	1.3×10^7
6 th day	10^{-6}	11	1.1×10^7
7 th day	10^{-5}	7	7×10^6

<u>GA</u>			<u>pfu/ml</u>
10 th day	10^{-4}	12	1.2×10^5
14 th day	10^{-4}	32	3.2×10^5
19 th day	10^{-4}	18	1.8×10^5

GA HEL 293 infected \bar{c} PM 975 did not CPE, but
it gave viral yield $\approx 10^4$

5th day is plaque assayed today 2/25/97
GA PM 975

EXHIBIT

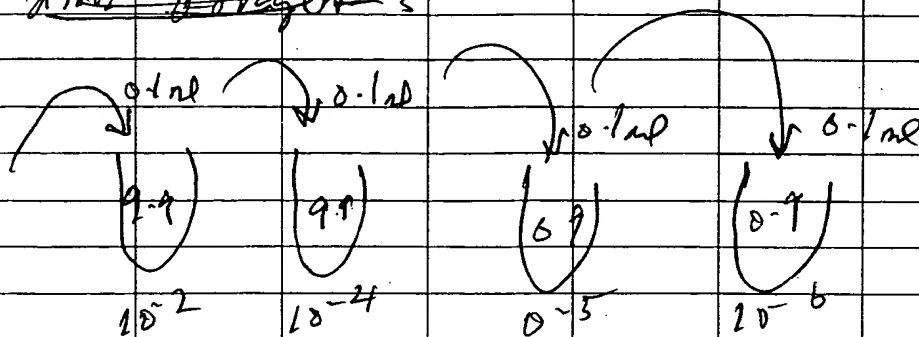
731

Growth curve:

3/5/97

pm 975 - growing 1 + 3rd log.

~~1102~~ ~~1000~~ 5th



EXHIBIT

452

Growth Curve: plaque assay

2111172

Growing:

G1 day d1 1101/1107
G2 (3 day) " /

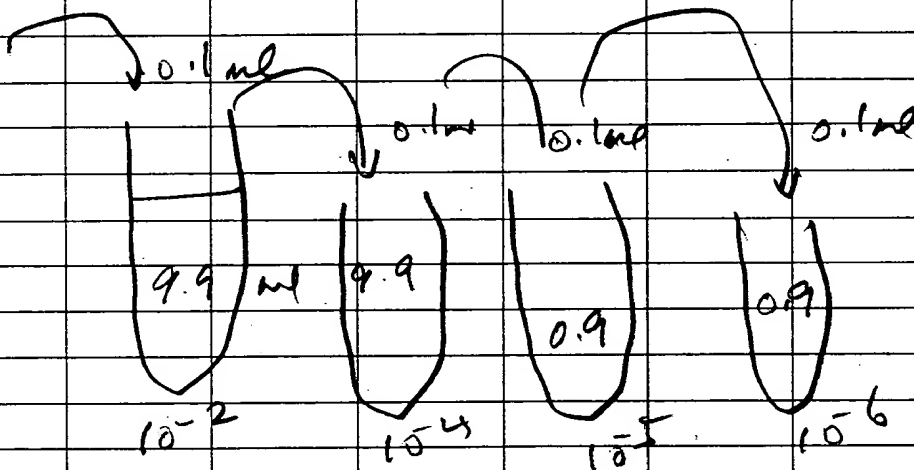
G1 d1 309
G5 d1 309

G A = G A1 d1 1101/1107 ;

G A1, d1 309
G A5 - d1 309
day

7 viases :

dilutions



551212

EXHIBIT

233

ST. S. Grand: Amco
867-6292
782-1089
989-3880

Growth Curve.

3.1.97

Growing: Day 1 (G2) ^{PA 975} = 4×10^{-4} 0.5ml 6th day infection
 = 4×10^4 = 8×10^4 / ml

Day 3

= 1.9×10^{-5}
 1×10^{-6}
 = 1.9×10^6

wait 2 more days.

↓ 0.5ml
 3.8×10^6 / ml

very small plaques.
 allow two more days to
 form more plaques.

↓
 31×10^6 (counted after 2 days)

↓
 3.1×10^7 PFU/ml

Growth arrested.

5/31/71

500 pfu

HEL 299 = 1 cells 351,000

1) for dil 1101/07
dilute virus to 10^9
(10 μ l to 1ml)

$$= \frac{5}{500} \times 351,000$$

$$= \frac{1.95 \times 10^4}{10^7} = 1.95 \times 10^{-3}$$

290 μ l ✓

2) for dil 309
dilute the virus to 10^9
(10 μ l to 1ml)

$$= \frac{5}{500} \times 351,000$$

$$= \frac{2.15 \times 10^4}{10^7} = 2.15 \times 10^{-3}$$

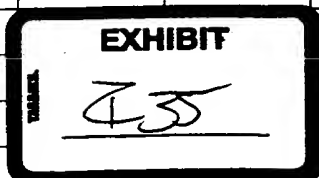
81 μ l ✓

↓
wash
infect, remove,
add EMEM + 0.2% FBS.

Freeze) 1 row 3/31/97 ✓

1 day
6
8
15

9
10
15
21



CPE Table

Growing (100 pm/cell) HEL 293 - P ¹⁷					
	d1309	pm975	d11101/107		
Day					
1	-	-	-		
3	+	+	-		
5	+++	+++	-		
6	++++	++++	-		
7			-		
10			-		
15			+	(cell morphology changes)	
24			++		

Growth arrested

Day					
1	-	-	-		
3	±	-	-		
5	+	±	-		
9	++	-	-		
10	+++	-	-		
19		+	-		
24		+	-		

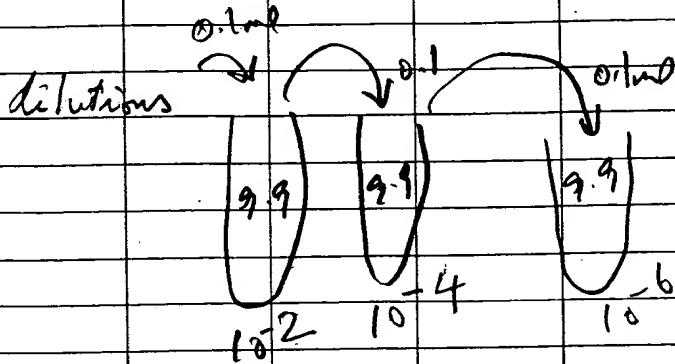
EXHIBIT

P.3p

Titer: 233 cells d1 309 GA HEL 29

01/25/11

d1 309 GA: 500 pfu/ml



3h, 1 d, 4, 6, 8 days.
1 6 & 15

EXHIBIT

237

HEL 299 cells

5/14/11
5/15/97
5/19/97

500 pfu/cell

Growing

d1309 d1101/07

3 hrs	9×10^3	2×10^4	-
1 day	1×10^4	4.2×10^4	-
4 "	1.6×10^7	1.2×10^5	-
8 " \rightarrow	2.3×10^7	1.4×10^5	-
10 "	7×10^6	2.4×10^5	7.1×10^5
15 "	-	2.5×10^5	$\rightarrow 2.2 \times 10^6$
21 "	-	3×10^6	$\rightarrow 4.6 \times 10^6$

Growth arrested:

3 hrs	8.9×10^3	4×10^4	-
1 day	6.1×10^4	4.4×10^4	-
4 "	6.2×10^5	4×10^4	-
8 " \rightarrow	1.3×10^6	5×10^4	5.2×10^4
10 "	9.2×10^6	1×10^4	1.6×10^4
15 "	-	1×10^4	1.4×10^4
21 "	5×10^5	2×10^4	2.2×10^4

$\approx 9 \times 10^3$

#4
Mohan
Wahid Bhat

EXHIBIT

I 38

7/12

① harvest flasks p 150
Ad 1
Ad III
Bailey

② freeze: 11-Q - ⑥
② 11-N - ⑥ 11-N - ③
11-M - ③ | split into (p 100)

As49 MT2 hygro (freeze)
msb - crmA ② (Freeze + split) (p 100)
11.b.11 (split 1:3) just a bit too heavy
crmA - 11.b ⑤ split (freeze)
11.b - crmA ⑨ split (freeze)

Bring up msb - crmA₂ to FLASK

3. Harvest virus spinner.

4. split other spinners.

My Spinner:

- 5.4×10^5 cells / ml
split $\frac{1}{2}$ - freeze cells

- 4.4×10^5 / ml / 1 ltr removed
and frozen

EXHIBIT

K1

8 - 100MM

7/13

todo

phone:

Ab in white/red File on Arms desk

Inventory virus bank * label / ✓ ✓ ✓

✓ (KBS from freezer) / when brought up

$2 \times 10^5 / \text{ml}$

7.5×10^7

Develop the gel (Monday)

✓ (cells frozen & thrown out)

No less than 2×10^5
3mls / 250mls cell

(Lysate / media)

Ad 1 + Ad 6 Virus stock (5mls of stock)

Set up
1-100ml → stock
media.

grow up 11.6 pre-Absorbed. ✓ Set up

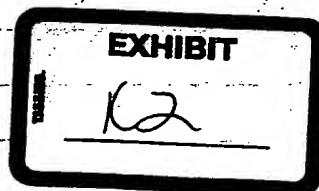
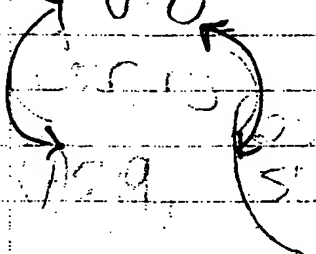
293 cells from Karyl (Diplo I) OK
Ginsberg H5d III (earliest stock) (175 flasks)

V9103 S-2-1 stock 50ul → 100mm plate → flasks

V9103 S-4-1 spin down / media 20% FBS 100ul → 100mm plate
(harvested) (960725)

Baylery 11/07/6 (911003) 104-8 loc. 50ul → 100mm plate

freeze thaw
harvested (960725) 104-8



1. spinner 1 liter K.B.'s

Count 3.4×10^5 cells/ml
split 500ml into a 3 liter flask add 1.5 liter
Jokke's media. Bring original 1 liter spinner
up to 1 liter (Jokke's + 10% hrs) serum)

2 3 liter spinner of K.B.'s infected

Count is 3.2×10^5 cells/ml
~~are~~ infect with (Baileys) 11/07/6 911003)

Baileys used was of a new stock grown up
in 293 cells. last week Baileys. 9600;
(Titer unknown) infected at 11:30 → 12:30

used 20ml of virus into 1 liter of cells
for 1 hour. then added back media
(2 liters Jokke's + 100 ml denatured
Horse serum)

3. develop gels.

4. split 293 give one plate to Ann. (split other cells)

5. look at plaques that are forming.
Very few now since yesterday
to count tomorrow.

EXHIBIT

K3

1. Split 293, A549 in 60mm (dishes)
2. Bring 3 liter spinner up to add 1 liter
count. 4.2×10^5

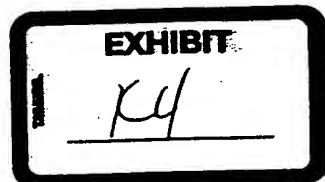
infect tomorrow w/ (704)

3. New media into all 56-29, 56-25, M56-2md,
M56-3md, CMA-56-3, 11.6-1md, 11.6 CMA-3 +
A54911-Q

4. Harvest infected spinner; Bailey, wash
pellet w/ PBS 2x (cold) resuspended it
into 24mls total vol of .01 M Tris pH 8.0
mls of cells + tris = 24mls
put into snap cap tubes & freeze at
-70°.
put in freeze (right inside Lindas lab)

5. Split + freeze 250-500mls of KB back up
Spinner.

6. Backup
Cells are not completely infected some
are dying so must harvest cells



CSC Banded the virus Ad1 960825
1101/1107 Baileys (960902)

- 1 freeze (thaw)
- 2 sonicate x 2
- 3 Vol after son 1101 < 21mls

Ad1 < 19mls

add $V \times 0.51 = g$ of CSC

10.71g in 1101/1107 Baileys
9.69g w Ad1.

infect 3 liter spinner with
dl 7/7 Vp 891208 Titer 1.3×10^8

cell count 3 liter 3.5×10^5
Vol = 3 liters (3000mls)

$3.5 \times 10^5 \times 3000\text{mls} = 10.5 \times 10^8$ total
cells

use 20 pfus / cell

$\frac{162\mu\text{l} = 0.105 \times 10^8}{1.3 \times 10^8} \times 20 \text{ pfus}$

KB's are healthy no clumping

EXHIBIT

K5

Black (first)

960			9/25	Plaque Assay		Comment
	Virus	Dil	A	B	C	
1.	1101/1107 (first infection)	5×10^{-6}	9	25	—	
		5×10^{-7}	3	1	—	
		5×10^{-8}	Ø	Ø	Ø	
		5×10^{-9}	Ø	Ø	Ø	
		5×10^{-10}	Ø	Ø	Ø	
2	765	5×10^{-6}	TMTCA			
		5×10^{-8}	3	Ø	Ø	
		5×10^{-9}	Ø	Ø	Ø	
		5×10^{-10}	Ø	Ø	Ø	
3	717	5×10^{-8}	Ø			Very hard to see plaques. today
		5×10^{-9}	Ø	Ø	Ø	
		5×10^{-10}	Ø	Ø	Ø	

EXHIBIT
K6

1101 / 1107

$.5 \times 10^6$
 $.5 \times 10^7$
 $.5 \times 10^8$
 $.5 \times 10^9$
 $.5 \times 10^{10}$

A

TMTCA
 42
 6
 1
 0

B

TMTCA
 53
 4
 0
~~0~~

C

8
 1
 0

Comments

small plgs. (flat)

717

$.5 \times 10^6$
 $.5 \times 10^8$
 $.5 \times 10^9$
 $.5 \times 10^{10}$

TMTCA
 TMTCA ←
 34
 1

28
 3

36
 3

hard to count
 because everywhere
 (very faint)
 v. small

765

$.5 \times 10^6$
 $.5 \times 10^8$
 $.5 \times 10^9$
 $.5 \times 10^{10}$

TMTCA
 12
 2
 0

19
 1
 0

1
 0

EXHIBIT

K7

1101/1107

1.5×10^6
 $.5 \times 10^{-7}$
 $.5 \times 10^8$
 $.5 \times 10^8$
 $.5 \times 10^{-10}$

A
 TMTC
 9
 14
~~8~~
~~8~~

B
 TMTC
 14
 14
~~8~~
~~1~~

C
 12
~~8~~
~~8~~

Comment
 start off small
 grow very
 quickly

717

1.5×10^{-6}
 $.5 \times 10^{-8}$
 1.5×10^{-9}
 $.5 \times 10^{-10}$

TMTC
 TMTC
 59
 4

45
 4

55
 8

Very very
 small

765

1.5×10^{-6}
 $.5 \times 10^{-8}$
 1.5×10^{-9}
 $.5 \times 10^{-10}$

TMTC
 9
 2
 1

11
 3
~~8~~

3 monolayer
 strong

EXHIBIT

K8

1101/1107

1.5×10^6
 $.5 \times 10^{-7}$
 $.5 \times 10^8$
 $.5 \times 10^9$
 $.5 \times 10^{-10}$

A

TmTC
 all together hard

5
 \emptyset
 \emptyset

B

mold + tmtc
to count

7
 \emptyset
 \emptyset

C

2
 \emptyset
 \emptyset

Comment

717

1.5×10^{-6}
 $.5 \times 10^{-8}$
 1.5×10^{-9}
 $.5 \times 10^{-10}$

TmTC
 TmTC
 14
 5

—
 TmTC
 13
 4

—
 7
 10

small
but visible

765

1.5×10^{-6}
 1.5×10^{-8}
 1.5×10^{-9}
 1.5×10^{-10}

TmTC
 5
 1
 1

3
 2
 mold

3
 1

EXHIBIT

K9

1101/1107

1.5×10^6
 1.5×10^{-7}
 1.5×10^8
 1.5×10^9
 1.5×10^{10}

A

TmTC
 TmTC
 no new aed \emptyset
 \emptyset
 \emptyset

B

TmTC
 \emptyset
 \emptyset
 \emptyset

C

TmTC
 \emptyset
 \emptyset

Comment

717

1.5×10^6
 1.5×10^8
 1.5×10^9
 1.5×10^{10}

TmTC
 TmTC
 TmTC
 3

TmTC
 TmTC
 \emptyset

TmTC
 2

765

1.5×10^6
 1.5×10^8
 1.5×10^9
 1.5×10^{10}

TmTC
 \emptyset
 \emptyset
 \emptyset

2
 \emptyset

throw out

mono layer
 gene
 \emptyset
 \emptyset

EXHIBIT

K10

1101/1107

1.5×10^6
 $.5 \times 10^{-7}$
 $.5 \times 10^8$
 $.5 \times 10^9$
 $.5 \times 10^{10}$

A	B	C	Comment
TMTCA			
7	2		
3	5	6	
0	0	0	
0	0	0	

Plg camp
 up quickly
 then tapered
 off.

717

1.5×10^{-6}
 $.5 \times 10^{-8}$
 1.5×10^{-9}
 $.5 \times 10^{-10}$

TMTA
 TMTA
 16
 3

TMTA
 17
 4

19
 7

765

1.5×10^{-6}
 $.5 \times 10^{-8}$
 1.5×10^{-9}
 $.5 \times 10^{-10}$

TMTCA
 5
 1
~~0~~

3
~~0~~
~~0~~

~~0~~
~~0~~

EXHIBIT

K11

1101/1107

 1.5×10^6 1.5×10^{-7} 1.5×10^8 1.5×10^9 1.5×10^{10}

A

TMTC

TMTC

+1

+0

0

B

TMTC

TMTC

+2

0

~~X~~

C

—

—

+0

+0

0

Comment

717

 1.5×10^{-6} 1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}

TMTC

TMTC

TMTC

+0

—

—

+2

—

—

+0

765

 1.5×10^{-6} 1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}

TMTC

+1

+0

+1

—

+1

+0

+0

—

—

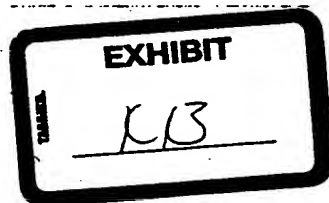
+0

—

EXHIBIT

K12

	A	B	C	Comment
1101/1107 1.5×10^6 $.5 \times 10^{-7}$ $.5 \times 10^8$ $.5 \times 10^9$ $.5 \times 10^{-10}$	mold tmtc 5 \emptyset \emptyset	34 blended together tmtc 4 \emptyset \emptyset	9 \emptyset \emptyset	Really big
765 1.5×10^{-6} $.5 \times 10^{-8}$ 1.5×10^{-9} $.5 \times 10^{-10}$	tmtc tmtc 4 \emptyset	3 \emptyset	12 \emptyset	Monolayer looks bad no new just bigger
768 1.5×10^{-6} $.5 \times 10^{-8}$ 1.5×10^{-9} $.5 \times 10^{-10}$	tmtc tmtc tmtc 3	tmtc tmtc \emptyset	2	



		A	B	C	comment
760	5×10^{-8} 5×10^{-9} 5×10^{-10}	TMTZ 37 3	TMTZ 29 1	TMTZ 26 4	
327	5×10^{-8} 5×10^{-9} 5×10^{-10}	TMTZ 60 18	TMTZ 74 17	74	
1101/1107	5×10^{-6} 5×10^{-7} 5×10^{-8} 5×10^{-9} 5×10^{-10}	TMTZ TMTZ TMTZ 66 8	TMTZ TMTZ TMTZ 64 17	70	Bg alpp
702	5×10^{-8} 5×10^{-9} 5×10^{-10}	TMTZ TMTZ 36	TMTZ TMTZ 30	TMTZ 36	

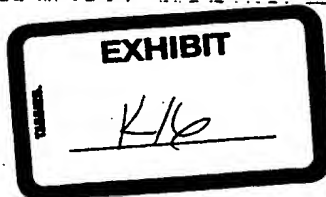


		A	B	C	comment
760	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TmTC 44 5	TmTC 40 4	TmTC 42 6	
327	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TmTC 64 <i>really twice</i> 18	TmTC 74 16	72 37 <i>missed counting first time</i>	
1101/1107	$.5 \times 10^{-6}$ $.5 \times 10^{-7}$ $.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TmTC TmTC TmTC 25 11	<hr/> 21 9	22	<i>med nice plg.</i>
702	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TmTC almost <i>almost</i> 15	TmTC 24 14	22 15	

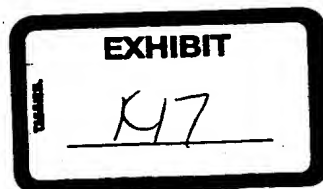
EXHIBIT

K15

		A	B	C	Comment
760	1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}	TMTc 10 1	TMTc 20 3	TMTc 15 1	small
327	1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}	TMTc TMTc 10	TMTc TMTc 8	TMTc TMTc 9	
1101/1107	1.5×10^{-6} 1.5×10^{-7} 1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}	TMTc TMTc TMTc 4 0	— TMTc TMTc 5 0	4 —	
702	1.5×10^{-8} 1.5×10^{-9} 1.5×10^{-10}	TMTc TMTc 3	TMTc 3	5	



		A	B	C	Comments
760	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TMTCA TMTCA 4	TMTCA TMTCA 3	3 1	very small easy to count.
327	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TMTCA TMTCA 3	TMTCA TMTCA 5	— TMTCA 6	
1101/1107	$.5 \times 10^{-6}$ $.5 \times 10^{-7}$ $.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TMTCA TMTCA TMTCA 0 2	— TMTCA TMTCA 1 1	0 0	Very Acidic
702	$.5 \times 10^{-8}$ $.5 \times 10^{-9}$ $.5 \times 10^{-10}$	TMTCA TMTCA 1	TMTCA 0	TMTCA 1	Very close hard to count



Keep plate 5×10^{-10} 760, 327
still growing pla

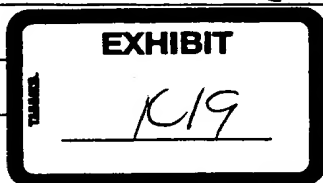


		Plaque Assays (% of final plaque #)							
	Virus	5d	7d	12d	13d	16d	19d	25d	30d
①	1101/1107	0.	18.3	55.	67.9	80.7	80.7	83.5	100.9
②	sub 765	2.6	32.8	57.8	65.5	79.3	81.	83.6	100.
③	dl 717	0.	10.3	33.8	54.4	82.4	89.7	92.6	100.

titer of 1101/1107 : 6.61×10^9 /ml
(harvested from KB cells at day 2)

		10-15-96 Plaque Assays (% of final plaque #)				
	Virus	8d	10d	13d	16d	21d
①	pm 760	32.4	78.	94.2	97.7	100.9
②	dl 327	32.1	65.4	82.1	90.7	100.
③	dl 1101/1107	65.7	94.6	98.7	100.	100.
④	dl 702	64.2	91.8	98.7	100.	100.

titer of 1101/1107 : 1.95×10^{11} pfu/ml
(harvested from KB cells at day 3)



	Virus	From	INF	Harvest	Spin	plaq	Comments	Freezer/6
1.	Ad4A9K	(VS58)	961016	961018				
2.	Ad4AE ₃	(96103)	961104	961106				
3.	Ad4AE ₃ B	(VS56)	961031	961102				
4.	1101/1107	(Baileys)	960905	960907	✓	✓		1-1
5.	1101/1107	2nd batch	960917	960919	✓	✓		1-1
6.	d1702	(VS33)	961002	V2day	✓	✓		1-2
7.	d1773	(VS230)	960909	V2day	✓			101-5
8.	d1717	(VS118)	960906	960908	✓	✓		2-2
9.	327	(VS212)	960914	960917	✓	✓		5-5
10.	Ad16D	(VS227)	960915	960917	✓	✓		4-6
11.	Ad 5	(VS198)	960907	960908	✓	✓	Great bands	101-2
12.	Ad 1	(sup)	960905	960907	✓	✓		2-1
13.	d1762	(Repeat)	961008	961008	✓	✓	Bad No plaques	2-3
14.	Ad 11	Sup	961030	961002				
15.	dL797	(VS243)	960929	960924				
16.	Ad 3						first spinn	
17.	Ad 6	SUP	960801	960803	✓	✓	Good bands	101-2
18.	Ad 9	(sup)	970209					
19.	dL703	VS50	961001	961003	✓			
20.	dL704	(VS167)	960802	960804	✓	✓	thin bands	5-2
21.	dL748	(VS181)	960708	960810	✓	✓		13-6
22.	dL798	(VS188)	960708	960710	✓	✓	Good	13-4
23.	dL763	(VS214)	960703	960705	✓	✓	Bad Bands look good	2-3
24.	dL765	(VS225)	960824	960826	✓	✓		101-8
25.	dL739	(VS223)	961023	just plq	✓	✓		
26.	dL754	(VS242)	960202	just plq	✓	✓		
27.	dL712	?	950503	—	✓	✓	Plays good	
28.	7001	?	960724	960726	✓	✓		
29.	dL250	sup	950616	950618	✓	✓	Big plaques / nice bands	
30.	Ad 41	Sup/293	(293)	→				
31.	Ad 40	Sup/293	(293)	→				
32.	Ad 707	(VS212)	961008	961110				
33.	Ad 740	VS240	960612					
34.	dL762	(Ad 29)	960120	961120			From 640620 see page	
35.	Ad 15	961024	970305		✓			
36.	Ad 11		970205	970205	✓	✓	Great bands	
37.	Ad 4		970205	970205	✓	✓	Great " " !	

EXHIBIT

K20

4/62
Chris

Low affinity Nerve growth receptor = .1 ug / ul

Viruses from Kostaya: grow in KB's first AB49
then KB.

= Viruses from Bowling: grow in AB49 first then
then in KB! 2 flasks

- set up 2 flasks for bowling virus. pmt 11/6
AAA

= KB's ready to infect in 3 liter spinner
count

- 1 liter being up to 1300 liters split
tomorrow.

dl 707: 1.57×10^{10}

count $3.8 \times 10^5 \times 9.9 \times 10^8$ cells / liter

$$\frac{0.99 \times 10^8}{1.57 \times 10^{10}} \times 10 \text{ PFU's} = .63 \text{ uO}$$
$$\frac{0.99 \times 10^8}{1.57 \times 10^{10}} \times 5 \text{ PFU's} = .315$$

Infect.

EXHIBIT

K21

4/28/monday

1. set up A549 for virus from Costag
2. split MCF-7 for transfection of
Nerve growth factor.
3. change media on MCF-7 - transfections
11.6 - MCF-7 ~ 5-6 clones per dish
MS6 - MCF-7 ~ 3-4 " "
except for one dish which has a lot more

thus:

set up transfection w/
low affinity Nerve growth factor

= 3 dishes
+ 11.6 = 3 dishes
2 controls

use new prep.

Coverslips of mcf-7.

ishaz Affinity Nerve growth factor .2 ug/ul

use

solution

$A = (PK \log FR MN) \cdot 2 \text{ ug/ul} = 25 \text{ ul/dish}$

NGF ONLY

3 NGF only

$A = 75 \text{ ul DNA} + 800 \text{ ul opti DMEM} =$

$B = 36 \text{ ul lip} + 1300 \text{ ul opti DMEM}$

A+B for 30 min 2.4 ml opti

NGF + 11.6

A

$5.7 \text{ 11.6} + 75 \text{ ul} + 300 \text{ ul opti DMEM}$

B

$36 \text{ ul lip} + 300 \text{ ul opti DMEM}$

A+B for 30 min 2.4 ml opti

2 dishes not transfected = for control

- mix A+B let sit R.T for 30 min, Add Raman-n media
- 1ml per dish / for five hours,
- then add 20% media (1ml) let incubate O/N
- stain tomorrow.

1 dish

$\text{pMT2 } 2.2 + 100 \text{ opti DMEM}$

$12 \text{ lipo} + 100 \text{ opti DMEM}$

Add 1ml 20% on transfection / Add 2% to infection

Set up flasks 293 (110 viruses)

Set up 4 A549 plates (100ul to pre absorb ab)

Add ~~car~~ Costas Virus to flasks - put

split 1/2 B/E

EXHIBIT

1623

5/2 Friday

- Freeze FAS cells - pool
- V infection
- split all cells /
- split KB's back

5/6 - split FAS to two flasks - for Kostya
- clones picked
- infect the other // spinner //

$$4.5 \times 10^5 \text{ cells/ml} / \times 3000 \text{ ml} =$$

13,500 cells.

Cells look ok: added 5 ml of
the virus 45.5 from Kostya to
the spinner

(Tomorrow pick clones.)
get cells from Mohan
make Jaklins media / ok

W



1:30

5/B

797?

freeze + thaw + spn to CS prep

viruses

sealign

20 mls

KD-1 1101/1107 ADP 970508

19 mls

PME 11.6 AAA

970508

20 mls

dl 707

970423

19 mls

dl 751

970324

Viruses in warm room X2 thaw.

~~gammac~~ also

20 mls

dl 707

970315

split A549 cells to Flasks for 797 + others
listed.

IN Freezer, need Sonicated in beater

location

PME = 1, 7

KD = 9, 3

751 = 11, 5

707 (970315) 8, 2

707 = 6, 12

set machine on
4° / 35K for
O/N ↔

EXHIBIT

K25

5/14

Viruses taken out of Centrifuge

(970508) ⁽⁴⁶⁻⁴⁷⁾ KD-1 (Kostya) 1101/1107 ADP: ^{harvest} ~ 4 mls (small thin bands)
(970324) dl 751 (nice thick bands) good = ~ 4 mls
(970315) dl 707 (very thick by bands great) = ~ 9 mls
(970423) dl 707 (nice bands) good = ~ 6 mls

(970503) PME-11.6 AAA (very nice bands) good ~ 5 mls/3
(BLY ADP-AAA)

(Note) Don't dilute KD-1 very much got alot of extra liquid w/ viruses band ~ 2 mls of actual virus.

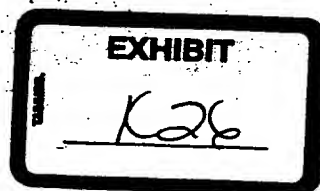
Dilute with TSB ~ 5x-10x

	tubes	LOC
KD-1 dilute bring up to (10 mls)	5	4-4
dl 751 bring up to (16 mls)	8	2-5
dl 707 (970315) bring up to (24 mls)	12	2-4
dl 707 (970423) bring up to (16 mls)	8	4-3
PME-11.6 AAA = bring up to (14 mls)	7	4-4
BLY (ADP-AAA)		

(plaque assay viruses) 751 original 53-3/60-B
one tube of each in my box to plaque 707 original

need to

infected 3 liter w/	HS dl 111	sup from flasks
3	HS dl 110	AS49
	dl 205	



5/20/97

assay. (Titer virus)

751 (970324)

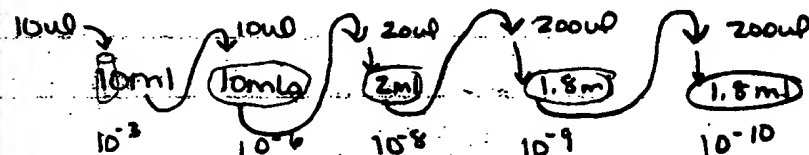
dl 707 (970315)

dl 707 (970423)

DME - 11.6 AAA (BLY-ADP-AAA) (970503)

KD-1 (970508) (Kostya)

dilute all viruses 10ul to 10mls (10^{-3} dilution)



2 - 10^{-8}

3 - 10^{-9}

3 - 10^{-10}

* each

50

5

2

1

43

100 mls 2x DME
10 mls Sodium Bi
4 mls FBS
2 mls Glut
80 mls AGAR

Add virus to the 3 liter spinner — dl 110 virus

3 liter Count: 4.2×10^5 cells/ml. use 1ml cells.

20110

1 liter Count: $(2.7 \times 10^5 \text{ cells/ml})$ split.

EXHIBIT

K27

6/2

and 9/23

	A	B	C
5×10^{-8}	TMTc	TMTc	/
5×10^{-9}	10	back	10
5×10^{-10}	2	✓	1

A	B	C
TMTc	TMTc	
9	5	10
3	0	0

707
(PMB)
Wagging

5×10^{-8}	14	15	/
5×10^{-9}	2	5	2
5×10^{-10}	0	0	0

68	47	
8	2	0
0	0	0

707

5×10^{-8}	13	15	/
5×10^{-9}	3	0	0
5×10^{-10}	0	0	3

30	17	
2	3	0
0	0	0

KD-7

5×10^{-8}	Total 162	163	Total 162
5×10^{-9}	Total 40	49	Total 49
5×10^{-10}	1	0	0

TMTc	TMTc	
3	1	1
1	0	2
	8.1×10^9	

PMB
(nice size
pregnancy)

5×10^{-8}	74	78	/
5×10^{-9}	16	11	20
5×10^{-10}	4	3	2

TMTc	TMTc	
12	14	7
1	0	2

EXHIBIT
K28

W138 infections with 1101/1107 and d1308

11/24

MOI	dividing	quiescent	549
0.1			
1			
10			
100			

16 35 mm W138
8 35 mm AS49 2.5×10^5 all/dish

infections 11/25
AS49 2.5×10^5 cells

5×10^4	0.1	
5×10^5	1	MOI
5×10^6	10	
5×10^7	100	

1.84×10^4
1101/107 (960917)
 3.8×10^5

5.8×10^2
10x dish 6pl

~~2.2 x 10³~~
~~312~~
~~1.8 x 10²~~
~~4pl~~

change medium on W138 to 0.2% FCS

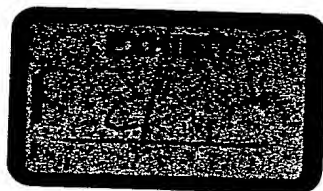
11/22 infect started W138 with

d308 (950511)

100
10 MOI
1
0.1

1101/1107 (960917)

100
10 MOI
1
0.1



ADP Western

infect A549 with 303, KDI 12/9

10^6 cells / dish 8.08×10^4 / ml $303 \Rightarrow 8.08 \times 10^4$ / ml
 $50 \mu\text{g}/\text{cell} \Rightarrow 6.18 \mu\text{l}$

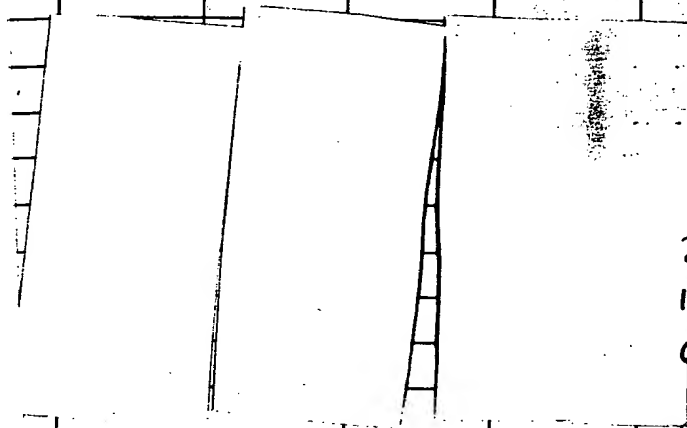
6.12×10^3 / ml $\text{KDI} \Rightarrow 6.12 \times 10^6$ / ml

$50 \mu\text{g}/\text{cell} \Rightarrow 8.16 \mu\text{l}$

Harvest 33h p.i.

ϕ	0.190		
mark	0.280	100	5 μl
303	0.359	173	2.8 μl
KDI	0.320	140	3.6 μl

4



100
173
140

10 and 15% SDS PAGE

[mark, 303, KDI] 3X, BR

transfer mark 12.5 10%, 456/5%

block 10% milk OV

cut 1st ab

4 12522II
 5 12531
 6 100578

1:400

2nd ab

3X

2nd ab

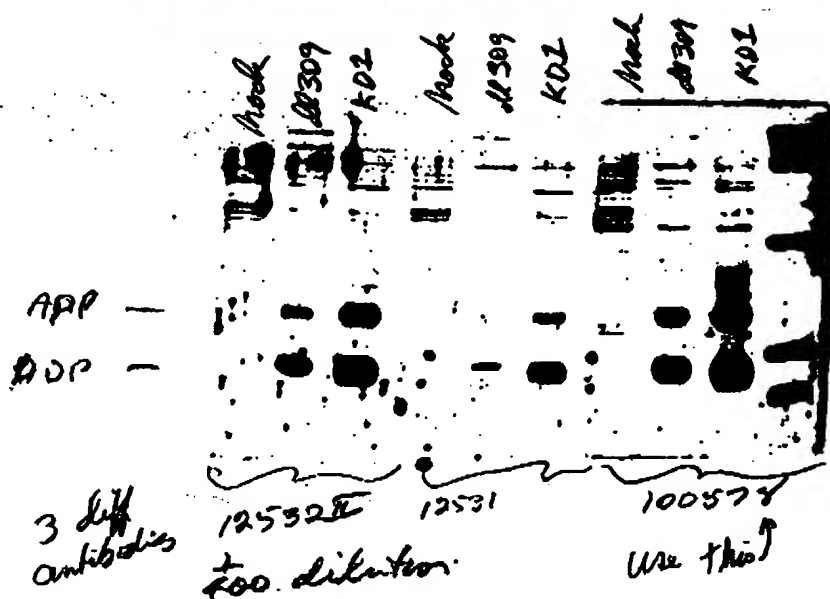
2 rabbit HRP

Wash

3X

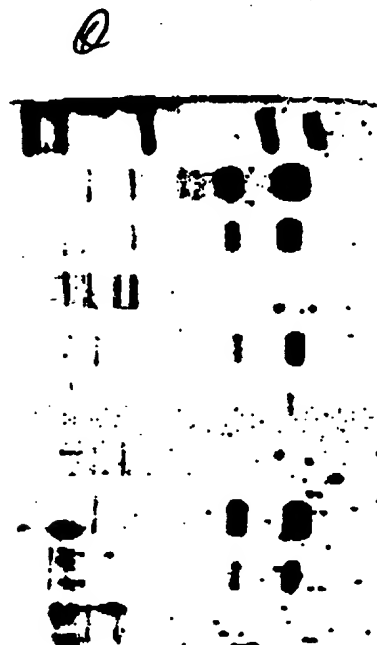


- KD1 expressed Ad5 Ab well
 - Can detect Ad5 by Western
 - Prelim - looks like KD1 expresses more ADP than 301?
 Used 500 PFA 7 KD1
 Used 50 PFA 7 KD1



ADP Western
 301 & 302

Next Sept - Time course
 KD1
 KD2
 KD3
 1101/1107



12/12/87



WDI

309

mod

WDI

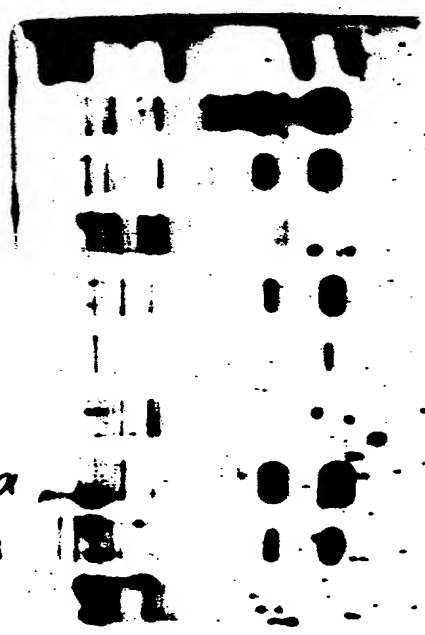
309

mod

WDI

309

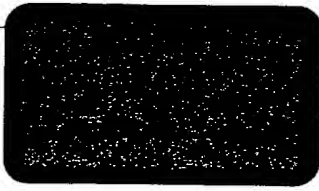
mod



100574

12531

12552





Certify that the document and fee is being deposited on 01/06/03 with the U.S. Postal Service as Express Mail under 37 C.F.R. 1.10 and is addressed to the Assistant Commissioner of Patents, Washington, D.C. 20231.

Express Mail No. EL474165334US

Daniel S. Kasten 1/6/03
Signature of Person Mailing Correspondence

Daniel S. Kasten
Typed or Printed Name of Person Mailing Correspondence

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Wold et al.	Group No.:	1632
Serial No.:	09/351,778	Atty. Docket No.:	66153-7775
Filed:	07/12/1999		
For:	Replication-Competent Anti-Cancer Vectors	Examiner:	Priebe, Scott David

DECLARATION, PURSUANT TO 37 C.F.R. §1.131,
OF WILLIAM S.M. WOLD, Ph.D., ANN E. TOLLEFSON, Ph.D., KONSTANTIN
DORONIN, Ph.D. AND KAROLY TOTH, D.V.M.

We, William S.M. Wold, Ph.D., Ann E. Tollefson, Ph.D., Konstantin Doronin, Ph.D. and Karoly Toth, D.V.M., declare and state as follows:

1. All of the statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true.

2. We are co-inventors of the inventions described and claimed in the above referenced patent application, filed July 12, 1999.

3. We conceived of a recombinant adenovirus vector which is replication-competent in neoplastic cells and which overexpresses an adenovirus death protein prior to March 3, 1997. We worked diligently, continuously and uninterrupted from prior to March 3, 1997, until we reduced the recombinant adenovirus to practice. The information contained in the documents of the attached exhibits was contemporaneously recorded on the dates indicated therein. Further, those exhibits are

true copies of the originals except to the extent that certain sensitive dates have been redacted. All noted dates that have not been redacted are accurate.

4. Claim 1 of the '778 application is directed to a recombinant adenovirus vector that is replication-competent in neoplastic cells and that overexpresses adenovirus death protein (ADP).

5. On or before March 3, 1997, we conceived of a recombinant adenovirus vector that is replication-competent in neoplastic cells and that overexpresses ADP, as evidenced by the activities set forth below. Unless otherwise noted, all of the documents referred to in the bullet point sections below are dated prior to March 3, 1997:

- Our early work focused on the E3 transcription unit (also referred to as the E3 region) of Adenovirus (Ad), and understanding the function of the various proteins encoded by that region. We observed that Ad comprising an ADP (11.6K) mutation (i.e. a mutation in the gene coding for ADP) developed plaques slower, and that those plaques were smaller, than Ad with wild type levels of ADP expression (see Exhibit A, page 1 [A1], where dl712 is an ADP mutant and Ad5 is a wild-type adenovirus).
- In addition, we observed that some mutant Ads that have portions of the E3 region deleted, other than the gene for ADP, produced larger plaques than the wild-type Ad. See page 2 of Exhibit A (page A2), which is a notebook page memorializing these observations. This page shows that dl753 produced larger plaques than wild-type.
- Plaque development assays indicated that ADP mutant Ad produced plaques at different rates than wild type Ad (see pages A3-A17, which are plaque assay results which show that dl753 and dl732 produce plaques faster than wild type Ad, and ADP deletion mutants form plaques slower than wild-type). Note that "rec700" represents wild-type Ad, and "dl 753" and "dl 732" are adenoviruses that have deletions in the E3 region [not in the open reading frame for ADP] that result in increased synthesis of ADP; and dl712, dl801, dl742, dl708 and dl7001 have deletions in the coding region for ADP that preclude synthesis of functional ADP.
- Gel electrophoresis studies were carried out which indicated that E3 deletion Ad produced higher levels of ADP (see Exhibit A, pages A18-A20, which are photocopies of those gels that show that dl753 (an E3 deletion mutant) produces more ADP than rec700 (which produces wild-type levels of ADP).
- Immunofluorescence assays were carried out that confirmed these findings that E3 deletion mutants produce more ADP than wild-type (See Exhibit A, pages A21-A25, where dl732 and dl753 are E3 deletion mutants that overexpress ADP, dl712 is an E3 mutant in which the gene for ADP is deleted, and rec700 is wild-type).

- In virus release assays, we observed that the ADP mutants that had large plaques released more virus than both wild-type Ad and ADP mutants that had small plaques (A26).

- This early work led us to hypothesize that ADP is required for cell lysis, and release of Ad. We also hypothesized that over-expression of ADP may cause cell lysis more rapidly, and therefore, that vectors that overexpress ADP may be useful as anti-cancer agents.

- A proposal, entitled "Adenovirus E3-11.6K Protein as a Cell Death-Promoting Agent," was sent to Dr. Rae Lyn Burke of Chiron Corp. That Proposal is submitted herewith as Exhibit B. At page 7 of that proposal, the concept of overexpressing ADP (11.6K) is discussed. Further, at page 4 the KD/GZ class of adenovirus vectors are described, where it is stated that "[t]he nondefective vectors generally have the E3 transcription unit deleted and replaced with the transgene" [e.g., ADP]. The concept that deletion of the E3 transcription unit and insertion of the ADP gene would result in overexpression is based on the understanding that deletion of most or all of the E3 genes other than the ADP gene facilitates overexpression of ADP mRNA by reducing competition for splicing of the major late pre-mRNAs. That concept is put forth in the instant specification at page 15, lines 12-17. That concept is also discussed in the proposal at page 7, where it is stated that "...we will determine whether 11.6K overexpressed during early stages of infection can promote cell death. The 11.6K gene will be built into our mutant, dl7001, which lacks the entire E3 region but expresses all other adenovirus genes... Cells will be infected with the dl7001-11.6K vector...and cell death will be monitored."

6. Prior to March 3, 1997, we constructed a recombinant adenovirus vector that is replication-competent in neoplastic cells and that overexpresses ADP. Specifically, KD1 is a recombinant adenovirus vector that is replication-competent in neoplastic cells and that overexpresses ADP. KD1 was constructed by cotransfecting dl1101/1107 DNA that had been digested with EcoRI and plasmid p54 DNA comprising the ADP gene into 293 cells. DNA from resulting plaques was confirmed as KD1 by PCR. The following activities, which occurred prior to March 3, 1997 are related to the construction and evaluation of ADP overexpressing vectors generally, and specifically KD1:

- High titer dl1101/1107 stocks were expanded for the purpose of examining whether this virus with a mutation in the E1A gene would grow well on cancer cell lines and not on non-cancerous cell lines, and also for the purpose of deleting the E3 region of an Ad strain and inserting the ADP from Ad5. (See Exhibit D1) (dl1101/1107 serves as the "backbone" of the KD strains described in the 09/351,778 application, see page 22, Table 1).

- High titer dl1101/1107 stocks were confirmed. (D2-D3).
- The EcoRI-A fragment of Ad5 containing the DNA sequence encoding ADP was purified. (D4)
- Various deletions and insertions were made in the backbone adenoviral E3 region by PCR. For example, in the construction of KD1, the ADP gene was isolated from the Ad5 genome by PCR using the primers named KD6 and KD7 that added PacI restriction sites to the DNA fragment containing the ADP gene. (E3, E4 and E9). This ADP-containing PCR fragment was cloned into a PacI site in the plasmid named pL2 to produce the shuttle plasmid named p54 (F7-F8) (D9). Another name for plasmid pL2 is pLKHE2A + Bam → end + Cla. The sequences for primers KD6 and KD7 are presented in Appendix E1, E3, E4 and E9 and are described in the '778 application. These primers as well as other primers were purchased from Gibco BRL. Exhibit E comprises order sheets and certificates of analysis for a number of those primers, along with contemporaneous notes that describe the primers. (E1-E10)
- Growth curves to assess whether dl1101/1107 is attenuated for growth as compared to dl309 in HEL299 cells. (I1-I31)
- Various plasmids used to construct the KD vectors were sequenced. (F1-F8)
- The DNA sequence of the ADP gene inserted into plasmid p54 was determined using the KD6 and KD7 primers (F7-F8)
- The ADP gene was successfully subcloned into the shuttle plasmid vector, culminating in the isolation of the KD1 shuttle plasmid vector. (Exhibit F5-F6) (D9)
- dl1101/1107 DNA that had been digested with EcoRI was cotransfected into 293 cells together with plasmid p54 DNA. (D39)
- Seven putative KD1 plaques from the above transfection experiment were observed. (C1) (KD) (WW) DNA from these plaques is confirmed as KD1. (C6)
- New DNA was prepared from cells infected separately with viruses isolated from ten plaques that resulted from the above co-transfection experiment. (C6)
- The above DNA was analyzed by restriction enzyme digestion and PCR. Three of the plaques were shown to contain the E3 region from plasmid p54; that is, three of the plaque isolates were KD1. (C9) (D48-49)
- A second cotransfection experiment was performed using EcoRI-digested dl1101/1107 DNA plus plasmid p54 in a repeat attempt to construct KD1. (D47). On 3/6/97 the Hirt supernatant DNA from four plaque isolates had been analyzed by PCR;

three of the plaque isolated had the E3 region of KD1. (D52) (C16). Thus, prior to March 3, 1997, KD1 had been constructed in two separate experiments.

7. From the time the KD1 vector was made, we continued to work on construction and characterization of additional replication competent vectors that overexpress ADP, as evidenced by the activities listed below. This work eventually led to the KD3, GZ1 and GZ3 vectors described in the specification of the '778 patent, particularly in the Examples. Our experiments show that KD1 overexpresses ADP. Specifically, on or about May 20, 1997, we show that KD1 develops plaques faster than dl309, which expresses wild-type levels of ADP. Faster plaque development is correlated with overexpression of ADP. Based on the plaque development assay, we concluded that KD1 overexpresses ADP. In addition to the activities listed below, certain activities occurred on a continual basis. Those activities include, among others, maintenance of stocks of human cell lines used in evaluating the vectors; maintenance of bacterial cell cultures used to generate stocks of the various plasmids used to construct the claimed vectors; experiments such as virus growth curves, virus plaque assays, virus spread assays, virus induced cell death assays, all of which require multiple days to complete; lab meetings and informal discussions of progress and strategies for future experiments. The following activities are evidence of our continuous efforts:

3/3/97-3/7/97:

- From prior to March 3, 1997 through at least March 7, 1997, plaque assays of KD1 (also referred to as 544 in the attached exhibits) continued to progress and observations were made. Also, stocks of cells comprising the recombinant virus with the E3 region deleted and ADP inserted were maintained. (C15-16)

- On 3/6/97 the Hirt supernatant DNA from four plaque isolates from the second cotransfection experiment performed using EcoRI-digested dl1101/1107 DNA plus plasmid p54 had been analyzed by PCR; three of the plaque isolated had the E3 region of KD1. (D52) (C16) .

- Growth curves with dl1101/1107 and dl309 on HEL299 cells or WI38 cells continue. (I32)

3/7/97-3/14/97:

- Plaque assays of the KD1 vector continued. (C19)
- Virus growth assays continued on WI38 cells to assess the growth of dl1101/1107. (C20)
- Assays continue to assess dl1101/1107 and dl309 in growth arrested vs. growing HEL299 cells. (C21, 133-34)
- Initial stocks of the KD1 virus had been prepared. (C19)

3/14/97-3/21/97:

- The E4 promoter region of dl1101/1107 was sequenced to help in constructing an E4 promoter substituted virus. (C22)
- Virus growth assays continued on WI38 cells to assess the growth of dl1101/1107. (C23)
- Sequencing of plasmids used to construct the KD vectors continued using various primers. (F9-F12)
- Assays continued to assess dl1101/1107 and dl309 in growth arrested vs. growing HEL299 cells. (C24-25)

3/21/97-4/4/97:

- HEL299 growing and growth arrested cells are infected with dl1101/1107 and dl309 and virus growth assays are in progress. (C26, 135-36)
- dl1101/1107 extracted from WI38 permissive cells is titered. (C27)

3/21/97-4/11/97:

- dl1101/1107/EcoRI and p101 or p111 are cotransfected and cell cultures observed to identify plaques that may comprise the KD2 and KD3 vectors. (C28)

4/4/97-4/11/97:

- Growth assays with dl1101/1107 and dl309 continue in HEL299 cells. (C29)
- Titer experiments continue with dl1101/1107 extracted from WI38 cells. (C30)

4/11/97-4/18/97:

- Plaques with putative KD2 and KD3 virus are observed, and Hirt preps of DNA from those plaques are made. (C31)

- Titer experiments continue with dl1101/1107 extracted from WI38 cells, and preliminary data are collected. (C32)

- Growth curve experiments with dl1101/1107 and dl309 on growth arrested and growing HEL299 cells are continued and data are compiled. (C34-35)

4/18/97-4/25/97:

- PCR and restriction enzyme digestions are done to confirm KD2, and Hirt DNA preps are made for putative KD3 plaques. (C36)

- Titer experiments continued with dl309 and dl1101/1107 extracted from infected WI38 cells. (C37-39)

- Growth curve experiment was started with dl1101/1107 and dl309 viruses on MCF-7 human breast cancer cells. (C37)

- HEL299 cells infected with dl1101/1107 and dl309 are frozen for growth curve analysis. (C40)

- Sequencing of plasmids used to construct KD vectors continued using various primers. (F13-F17)

- Cell culture supernatant stock of KD virus is given to lab technician (SB) for preparation of a high titer CsCl-banded stock. (C36)

4/18/97-5/2/97:

- Titrations of virus extracted from HEL299 cells infected with dl1101/1107 and dl309 continues. (C45)

- Plaque development assay started with KD1 comparing it to dl309 (wild-type E1A, normal ADP expression), dl1101/1107 (E1A mutation, wild-type ADP expression), pm734.1 (wild-type E1A, no ADP expression), and dl7001 (wild-type E1A, no ADP gene). The cell lines used were 293 and A549 cells. (C41) (D90-D92). The results of this plaque assay are shown graphically at C56. The KD1 and dl309 plaques developed approximately 2 to 3 days faster than did the plaques of dl1101/1107. The fact that KD1 plaques developed more rapidly than those of dl1101/1107 indicates that KD1 overexpresses ADP.

- SB (lab technician) obtained the KD1 virus from KD and began experiments to expand the amount of virus. (K21)

4/25/97-5/2/97:

- KD3 vector (referred to as dIE3Xba + ADP) was confirmed by PCR and restriction enzyme digestion. (C41)
- Experiments to expand KD1 continue. (K22 K23)

5/2/97-5/9/97:

- Stocks of dIE3 + ADP were grown and monitored for plaque development. Also, cells transfected with KD1, KD2 and KD3 are monitored for development of plaques relative to dl309. (C47, C49)
- Growing and growth arrested dl1101/1107 infected HEL299 cell extracts are titrated for growth curve. (C50)
- Expansion of KD1 continues. (K24) (C49)

5/9/97-5/23/97:

- Plaque development assays continue, to assess KD1, KD2 and KD3 relative to wild-type. (C51)
- Plaque assays to assess expression of ADP by KD1 relative to several viruses with wild-type E1A genes continue. Fast plaque formation by KD1 indicates ADP overexpression. (H2-H3)
- Growth curves with dl309 and dl1101/1107 extracted from HEL299 cells continue, and data is collected at various intervals. (C52-53)
- Sequencing of primers used to construct KD vectors continued. (F18-F19)
- Titering of dl309 DNA extracted from 293 cells is initiated. (I37)
- Growth curves with dl309 and dl1101/1107 extracted from HEL299 cells continue. (I38)
- Expansion of KD1 continues. (K25) (AT)

5/13/97-6/2/97:

- Plaque assay to assess KD1. Results indicate that KD1 overexpresses ADP. (K25-K28)

- Expansion of KD1 continues. (K26)

5/20/97-6/8/97:

- Plaque assays of various viruses including KD1 and dl751. (H4-H10). The plaque development curve indicates that KD1 formed plaques as well as or better than dl751, a virus that overexpresses ADP. This suggests that the virus had good ADP expression and function. (K27-28) (H4-H9). KD1 was plaque assayed along with dl751 (which expresses higher than normal quantities of ADP), two preparations of dl707 (a mutant in which a portion of ADP is deleted and which therefore would be expected to have delayed kinetics of plaque formation), and pm734.9 (an ADP mutant with a three amino acid mutation at the C-terminus of ADP [listed as PME on the plaque assay counts]).

5/23/97-5/30/97:

- Plaque development assays were monitored and results collected. C56 is a graphical presentation of results indicating that KD1 develops plaques as quickly as dl309 and quicker than dl1101/1107, and that KD2 and KD3 develop plaques more quickly than dl1101/1107. (C55-C58)

5/30/97-6/27/97:

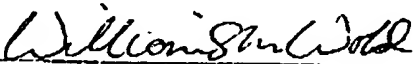
- Efforts focused on further characterization of the KD vectors, and improvements on those vectors, such as for example substituting the E4 promoter. Growth curves with dl1101/1107 continued, and Plaque development assays with KD1 indicated that KD1 develops plaques somewhat slower than dl309. (C65-C82)

- Infections were done for immunofluorescence staining for ADP. Viruses used for infection were dl309, KD1, KD2 and KD3. It is noted that KD shows much more staining for ADP than the other viruses (both at 27 and 49 hours post-infection). This is supporting data for the overexpression of ADP by the KD viruses. (H1-H2)

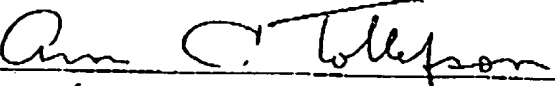
8. As evidenced by the foregoing, we confirmed that KD1 overexpresses ADP by Immunofluorescence assays utilizing an ADP-specific antibody on or about June 23, 1997.

9. We confirmed that KD1 overexpresses ADP by Western blot on or about December 1, 1997. (Exhibit L, pages L2-L4)

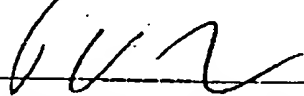
10. I understand that willful false statements and the like are punishable by fine or imprisonment, or both (18 U.S.C. 1001) and may jeopardize the validity of the application or any patent issuing thereon.




William S.M. Wold, Ph.D.



Ann E. Tollefson, Ph.D.



Karoly Toth, Ph.D. DVM KI



Konstantin Doronin, Ph.D.

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